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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 6, 2001, 09:42:17 ; Search time 14.27 Seconds  
(without alignments)  
14.377 Million cell updates/sec

Title: US-09-081-522-4  
Perfect score: 33  
Sequence: 1 GRDFV 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues  
Total number of hits satisfying chosen parameters: 26426

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: A.Geneseq-36.\*

- 1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT.\*
- 2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT.\*
- 3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT.\*
- 4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT.\*
- 5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT.\*
- 6: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT.\*
- 7: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT.\*
- 8: /SIDSI/gcgdata/geneseq/geneseq/AA1987.DAT.\*
- 9: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT.\*
- 10: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT.\*
- 11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT.\*
- 12: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT.\*
- 13: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT.\*
- 14: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT.\*
- 15: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT.\*
- 16: /SIDSI/gcgdata/geneseq/geneseq/AA1995.DAT.\*
- 17: /SIDSI/gcgdata/geneseq/geneseq/AA1996.DAT.\*
- 18: /SIDSI/gcgdata/geneseq/geneseq/AA1997.DAT.\*
- 19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT.\*
- 20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT.\*
- 21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	100.0	6	16	R82383	Peptide used for t
2	33	100.0	6	16	R82384	Peptide used for t
3	33	100.0	6	16	R82385	Peptide used for t
4	33	100.0	6	16	R82386	Cyclic integrin al
5	33	100.0	6	18	W33056	Alpha-V, beta-5 vi
6	33	100.0	6	19	W41096	Alpha-V beta-3 ant
7	33	100.0	6	19	W41097	Alpha-V beta-3 ant
8	33	100.0	6	19	W41098	Alpha-V beta-3 ant
9	33	100.0	6	19	W41099	Alpha-V beta-3 ant
10	33	100.0	6	19	W41242	Alpha-V beta-5 ant
11	30	90.9	6	16	R82393	Cyclic integrin al
12	30	90.9	6	19	W41105	Cyclic peptide 621

13	29	87.9	5	12	R11760	Peptide #4 having
14	29	87.9	5	13	R24515	Platelet antagonis
15	29	87.3	6	14	R69327	Gp IIB/IIIA recept
16	28	87.3	6	14	R69331	Gp IIB/IIIA recept
17	29	87.9	6	19	W52091	Targetting peptide
18	29	87.9	6	19	W52094	Targetting peptide
19	29	87.9	6	19	W50596	GPIIb/IIIa recepto
20	29	87.9	6	21	V54947	Peptide ligand for
21	29	87.3	5	15	V54951	Peptide ligand for
22	27	81.3	5	15	R45382	Cell adhesion inhi
23	27	81.3	5	15	R45384	Cell adhesion inhi
24	27	81.9	5	15	R45386	Cell adhesion inhi
25	27	81.8	5	15	R45387	Cell adhesion inhi
26	27	81.3	5	16	R82387	Cyclic integrin al
27	27	81.8	5	16	R82389	Cyclic integrin al
28	27	81.8	5	18	W33057	Alpha-V, beta-5 vi
29	27	81.3	5	18	W33055	Alpha-V, beta-5 vi
30	27	81.8	5	19	W41099	Alpha-V beta-3 ant
31	27	81.8	5	19	W41101	Alpha-V beta-3 ant
32	27	81.8	5	19	W41109	Alpha-V beta-3 ant
33	27	81.8	5	19	W41240	Alpha-V beta-5 ant
34	27	81.3	5	19	W41243	Alpha-V beta-5 ant
35	27	81.3	5	19	W41247	Alpha-V beta-5 ant
36	27	81.3	5	20	W92307	Cyclic azapeptide
37	27	81.3	6	15	R45370	Cell adhesion inhi
38	27	81.3	6	15	R45372	Cell adhesion inhi
39	27	81.3	6	15	R45374	Cell adhesion inhi
40	27	81.3	6	15	R45376	Cell adhesion inhi
41	27	81.3	6	15	R45377	Cell adhesion inhi
42	27	81.3	6	18	Y08057	Biotin derivative
43	26	78.3	5	12	R11757	Peptide #1 having
44	26	78.3	5	13	R24518	Platelet antagonis
45	26	78.3	5	15	R63576	Covalently binding

## ALIGNMENTS

RESULT 1	
ID R82383	standard: peptide: 6 AA.
AC R82383;	
DT 03-MAR-1996	(first entry)
DE Peptide used for the synthesis of integrin alpha-v-beta-3 inhibitors.	
XX	
XX Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;	
KW fibrinogen; inflammation; apoptosis; restenosis.	
OS Synthetic.	
XX	
XX Key	Location/Qualifiers
FT Modified-site	1
FT	/note= "BOC-Gly, the N-terminal is protected by a
FT	butyloxycarbonyl group"
FT	
FT Misc-difference	2
FT	/note= "D-Arg"
FT	
FT Modified-site	6
FT	/note= "Val-Ome, the C-terminal is protected by
FT	a methyl ester group"
XX	
XX W09525543-AL.	
PN	
PD 28-SEP-1995.	
XX	
XX 09-MAR-1995:	95WO-US03035.
PF	
XX 30-DEC-1994:	54US-0366665.
PR 18-MAR-1994:	94US-C210715.
XX	
PA (SCRI )	SCRIPPS RES INST.

XX Brooks P, Cheresh DA;  
 XX  
 XX WPI; 1995-344463/44.  
 XX  
 XX Inhibition of angiogenesis in a tissue, e.g. following angioplasty  
 PT - by admin. of a compn. comprising an alpha-v-beta3 antagonist,  
 PT useful for regression of established tumours, treating inflamed  
 PT tissue, etc.  
 XX  
 XX Example 1; Page 95; 135pp; English.  
 XX  
 XX The peptides R82383-85 are peptides used in the synthesis of a group  
 CC of inhibitor peptides of integrin alpha-v-beta-3. The inhibitor  
 CC peptides (R82386-96) may be administered in a compn. and are useful  
 CC for inhibition of inflamed tissue angiogenesis, e.g. that associated  
 CC with rheumatoid arthritis, retinal angiogenesis associated with  
 CC diabetic retinopathy, that associated with haemangioma, solid  
 CC tumours, or solid tumour metastases. The alpha-v-beta-3 antagonists  
 CC are also useful to induce apoptosis in neovasculature in a tissue.  
 CC The inhibitor peptides are pref. cyclic and contain an RGD sequence.  
 XX  
 XX Sequence 6 AA;  
 SO  
 Query Match 100.0%; Score 33; DB 16; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GRGDFV 6  
 DB 1 grgdfv 6  
 RESULT 2  
 ID R82384 standard; peptide: 6 AA.  
 XX  
 XX R82384;  
 XX  
 XX 03-MAY-1996 (first entry)  
 XX  
 XX Peptide used for the synthesis of integrin alpha-v-beta-3 inhibitors.  
 DE  
 XX Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;  
 KM fibrinogen; inflammation; apoptosis; restenosis.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note- "BOC-Gly, the N-terminal is protected by a  
 FT butyloxycarbonyl group"  
 FT  
 FT Misc-difference 2 /note- "D-Arg"  
 FT  
 FT  
 XX W09525543-A1.  
 XX  
 XX 28-SEP-1995.  
 XX  
 XX 09-MAR-1995; 95WO-US03035.  
 XX  
 XX 30-DEC-1994; 94US-0366665.  
 XX  
 XX 18-MAR-1994; 94US-0210715.  
 XX  
 XX (SCRI ) SCRIPPS RES INST.  
 XX  
 XX Brooks P, Cheresh DA;  
 XX  
 XX WPI; 1995-344463/44.  
 XX  
 XX Inhibition of angiogenesis in a tissue, e.g. following angioplasty  
 PT - by admin. of a compn. comprising an alpha-v-beta3 antagonist,  
 PT

PT useful for regression of established tumours, treating inflamed  
 PT tissue, etc.  
 XX  
 XX Example 1; Page 96; 135pp; English.  
 XX  
 XX The peptides R82383-85 are peptides used in the synthesis of a group  
 CC of inhibitor peptides of integrin alpha-v-beta-3. The inhibitor  
 CC peptides (R82386-96) may be administered in a compn. and are useful  
 CC for inhibition of inflamed tissue angiogenesis, e.g. that associated  
 CC with rheumatoid arthritis, retinal angiogenesis associated with  
 CC diabetic retinopathy, that associated with haemangioma, solid  
 CC tumours, or solid tumour metastases. The alpha-v-beta-3 antagonists  
 CC are also useful to induce apoptosis in neovasculature in a tissue.  
 CC The inhibitor peptides are pref. cyclic and contain an RGD sequence.  
 XX  
 XX Sequence 6 AA;  
 SO  
 Query Match 100.0%; Score 33; DB 16; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GRGDFV 6  
 DB 1 grgdfv 6  
 RESULT 3  
 ID R82385 standard; peptide: 6 AA.  
 XX  
 XX R82385;  
 XX  
 XX 03-MAY-1996 (first entry)  
 XX  
 XX Peptide used for the synthesis of integrin alpha-v-beta-3 inhibitors.  
 DE  
 XX Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;  
 KM fibrinogen; inflammation; apoptosis; restenosis.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 2 /note- "D-Arg"  
 FT  
 FT  
 XX W09525543-A1.  
 XX  
 XX 28-SEP-1995.  
 XX  
 XX 09-MAR-1995; 95WO-US03035.  
 XX  
 XX 30-DEC-1994; 94US-0366665.  
 XX  
 XX 18-MAR-1994; 94US-0210715.  
 XX  
 XX (SCRI ) SCRIPPS RES INST.  
 XX  
 XX Brooks P, Cheresh DA;  
 XX  
 XX WPI; 1995-344463/44.  
 XX  
 XX Inhibition of angiogenesis in a tissue, e.g. following angioplasty  
 PT - by admin. of a compn. comprising an alpha-v-beta3 antagonist,  
 PT useful for regression of established tumours, treating inflamed  
 PT tissue, etc.  
 XX  
 XX Example 1; Page 97; 135pp; English.  
 XX  
 XX The peptides R82383-85 are peptides used in the synthesis of a group  
 CC of inhibitor peptides of integrin alpha-v-beta-3. The inhibitor  
 CC peptides (R82386-96) may be administered in a compn. and are useful  
 CC for inhibition of inflamed tissue angiogenesis, e.g. that associated  
 CC with rheumatoid arthritis, retinal angiogenesis associated with



CC diabetic retinopathy, that associated with haemangioma, solid  
CC tumours, or solid tumour metastases. The alpha-v-beta-3 antagonists  
CC are also useful to induce apoptosis in neovasculation in a tissue.  
CC The inhibitor peptides are pref. cyclic and contain an RGD sequence.

XX  
SQ Sequence 6 AA;

Query Match 100.0%; Score 33; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDFV 6  
111111  
DB 1 grgdfv 6

RESULT 4  
R82386 standard; peptide; 6 AA.

XX  
AC R82386;  
DT 03-MAY-1996 (first entry)

XX Cyclic integrin alpha-v-beta-3 inhibitor peptide no. 62181.

XX Integrin: alpha-v-beta-3; inhibitor; angiogenesis; antagonist;  
KM fibrinogen; inflammation; apoptosis; restenosis; cyclic.

XX Synthetic.

OS  
FH Key Location/Qualifiers  
FT Misc-difference 2 /note="D-Arg"

XX W09525543-A1.

XX 28-SEP-1995.

XX PF 09-MAR-1995; 95WO-US03035.

XX PR 30-DEC-1994; 94US-0366665.

XX PR 18-MAR-1994; 94US-0210715.

XX PA (SCRI ) SCRIPPS RES INST.

XX PI Brooks P, Cheresh DA;

XX WPI; 1995-34463/44.

XX Inhibition of angiogenesis in a tissue, e.g. following angioplasty  
PT - by admin. of a compsn. comprising an alpha-v-beta3 antagonist,  
PT useful for regression of established tumours, treating inflamed  
PT tissue, etc.

XX Claim 4; Page 97; 135pp; English.

XX R82386-96 are a group of inhibitor peptides of integrin alpha-v-beta-3.  
CC The inhibitor peptides may be administered in a compsn. and are useful  
CC for inhibition of inflamed tissue angiogenesis, e.g. that associated  
CC with rheumatoid arthritis, retinal angiogenesis associated with  
CC diabetic retinopathy, that associated with haemangioma, solid  
CC tumours, or solid tumour metastases. The alpha-v-beta-3 antagonists  
CC are also useful to induce apoptosis in neovasculation in a tissue.  
CC The inhibitor peptides are pref. cyclic and contain an RGD sequence.

XX Sequence 6 AA;

Query Match 100.0%; Score 33; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDFV 6  
111111  
DB 1 grgdfv 6

RESULT 5  
W33056 standard; peptide; 6 AA.

XX W33056;

XX 26-JAN-1998 (first entry)

XX Alpha-v, beta-5 vitronectin receptor antagonist.

XX RGD containing peptide; antagonist; alpha-v, beta-5;  
KM vitronectin receptor; inhibition; angiogenesis; inflammation;  
KM rheumatoid arthritis; eye disease; diabetic retinopathy;  
KM age related macular degeneration; ocular histioplasmosis;  
KM retinopathy; prematurity; neovascular glaucoma;  
KM corneal neovascular disorder; transplantation; herpetic; luetic;  
KM keratitis; pterygium; neovascular pannus; haemangioma;  
KM solid tumour; metastasis; cytokine; low toxicity;  
KM vascular endothelial growth factor;  
KM transforming growth factor alpha; epidermal growth factor; cyclic.

XX Synthetic.

OS  
FH Key Location/Qualifiers  
FT Misc-difference 1 /note="D-form residue"

XX W09706791-A1.

XX 27-FEB-1997.

XX PF 13-AUG-1996; 96WO-US13194.

XX PR 14-AUG-1995; 95US-0514799.

XX PR 14-AUG-1996; 96ZA-0006886.

XX PA (SCRI ) SCRIPPS RES INST.

XX PI Brooks P, Cheresh DA, Friedlander M;

XX WPI; 1997-163013/15.

XX Inhibiting angiogenesis with an antagonist selective for the  
PT alpha-v-beta-5 integrin receptor - e.g. antibody, RGD peptide or  
PT organic mimetic, for treatment of inflammation, eye disease, tumours  
PT etc.

XX Claim 5; Page 105; 126pp; English.

XX The present RGD containing peptide is an antagonist of the alpha-v,  
CC beta-5 vitronectin receptor, which can be used to inhibit  
CC angiogenesis in alpha-v, beta-5 containing tissue, specifically  
CC angiogenesis as a result of inflammation (especially rheumatoid  
CC arthritis), eye disease (especially diabetic retinopathy, age  
CC related macular degeneration, ocular histioplasmosis, retinopathy of  
CC prematurity or neovascular glaucoma), corneal neovascular disorders  
CC (especially transplantation, herpetic or luetic keratitis,  
CC pterygium and neovascular pannus associated with wearing contact  
CC lenses), haemangioma, solid tumours and their metastases or  
CC cytokines (especially vascular endothelial growth factor,  
CC transforming growth factor alpha or epidermal growth factor). The  
CC antagonist has the advantage of being very specific, affecting no  
CC processes other than angiogenesis and therefore of relatively low  
CC toxicity.

XX Sequence 6 AA;

Query Match 100.0%; Score 33; DB 18; Length 6;  
 Best Local Similarity 100.0%; Pred No. 2.1e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDFV 6  
 |||||  
 1 grgdfv 6

Db 1 grgdfv 6

RESULT 6  
 ID W41096 standard; Peptide; 6 AA.  
 XX W41096;  
 AC W41096;  
 DT 08-JUN-1998 (first entry)  
 XX  
 DE Alpha-v beta-3 antagonist precursor peptide.  
 XX  
 KW Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;  
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;  
 KW diabetic retinopathy; macular degeneration; restenosis; therapy.  
 XX  
 OS Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT Modified-site 1 /note- "N-terminus protected by Boc"  
 FT MISC-difference 2 /note- "D-form residue"  
 FT  
 XX W09745137-A1.  
 PN  
 PD 04-DEC-1997.  
 XX  
 PE 30-MAY-1997; 97WO-US09158.  
 XX  
 PR 31-MAY-1996; 96US-0018733.  
 PR 31-MAY-1996; 96US-0015869.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Brooks P, Cheresch DA;  
 XX  
 DR WPI; 1998-032334/03.  
 XX  
 PT Packaging material containing polypeptide antagonist of alpha-v  
 PT beta3 integrin - used for inhibition of angiogenesis, and for  
 PT treating tumours, inflammation, eye diseases etc.  
 XX  
 PS Example 1; Page 47; 234pp; English.  
 XX  
 CC This synthetic RGD peptide was used in the preparation of a cyclic  
 CC peptide, designated 62181 (see W41098), that is an antagonist of  
 CC integrin alpha-v beta-3. An N- and C-terminally protected peptide  
 CC (see W41095) was dissolved in methanol to which 2 N NaOH solution  
 CC was added. The admixture was stirred for 3 hr at 20 degC. After  
 CC evaporation, the residue was taken up in water, acidified to pH 3  
 CC with diluted HCl and extracted with ethyl acetate. The peptide  
 CC product (see W41096), which has a free C-terminal carboxylic acid,  
 CC was stirred at 20 degC for 2 hr with 2 N HCl in dioxane to obtain a  
 CC further peptide (see W41097). This was treated with  
 CC dicyclohexylcarbodiimide, 1-hydroxybenzotriazole and  
 CC N-methylmorpholine to produce the cyclic peptide. The invention  
 CC relates to the discovery that angiogenesis is mediated by the  
 CC specific vitronectin receptor alpha-v beta-3, and that inhibition  
 CC of alpha-v beta-3 function inhibits angiogenesis. Claimed  
 CC antagonists of alpha-v beta-3 comprise C-terminal fragments (see  
 CC W41083-94) of human or chicken matrix metalloproteinase-2,  
 CC polypeptides, cyclic or linear polypeptides, derivatised  
 CC polypeptides, a monoclonal antibody or organic mimetic compound.

Sequence 6 AA:  
 Query Match 100.0%; Score 33; DB 19; Length 6;  
 Best Local Similarity 100.0%; Pred No. 2.1e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDFV 6  
 |||||  
 1 grgdfv 6

Db 1 grgdfv 6

RESULT 7  
 ID W41097 standard; Peptide; 6 AA.  
 XX W41097;  
 AC W41097;  
 DT 08-JUN-1998 (first entry)  
 XX  
 DE Alpha-v beta-3 antagonist precursor peptide.  
 XX  
 KW Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;  
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;  
 KW diabetic retinopathy; macular degeneration; restenosis; therapy.  
 XX  
 OS Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT MISC-difference 2 /note- "D-form residue"  
 FT  
 XX W09745137-A1.  
 PN  
 PD 04-DEC-1997.  
 XX  
 PE 30-MAY-1997; 97WO-US09158.  
 XX  
 PR 31-MAY-1996; 96US-0018733.  
 PR 31-MAY-1996; 96US-0015869.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Brooks P, Cheresch DA;  
 XX  
 DR WPI; 1998-032334/03.  
 XX  
 PT Packaging material containing polypeptide antagonist of alpha-v  
 PT beta3 integrin - used for inhibition of angiogenesis, and for  
 PT treating tumours, inflammation, eye diseases etc.  
 XX  
 PS Example 1; Page 47; 234pp; English.  
 XX  
 CC This synthetic RGD peptide was used in the preparation of a cyclic  
 CC peptide, designated 62181 (see W41098), that is an antagonist of  
 CC integrin alpha-v beta-3. An N- and C-terminally protected  
 CC peptide (see W41095) was dissolved in methanol to which 2  
 CC N NaOH solution was added. The admixture was stirred for 3 hr at  
 CC 20 degC. After evaporation, the residue was taken up in water,  
 CC acidified to pH 3 with diluted HCl and extracted with ethyl acetate.  
 CC The peptide product (see W41096), which has a free C-terminal  
 CC carboxylic acid, was stirred at 20 degC for 2 hr with 2 N HCl in  
 CC dioxane to obtain a further peptide (see W41097), which has free  
 CC N- and C-terminals. This was treated with dicyclohexylcarbodiimide,  
 CC 1-hydroxybenzotriazole and N-methylmorpholine to produce the cyclic  
 CC peptide. The invention relates to the discovery that angiogenesis  
 CC is mediated by the specific vitronectin receptor alpha-v beta-3,  
 CC and that inhibition of alpha-v beta-3 function inhibits angiogenesis.  
 CC Claimed antagonists of alpha-v beta-3 comprise C-terminal fragments  
 CC (see W41083-94) of human or chicken matrix metalloproteinase-2,  
 CC fusion polypeptides, cyclic or linear polypeptides, derivatised  
 CC polypeptides, a monoclonal antibody or organic mimetic compound.

SQ Sequence 6 AA:

Query Match 100.0%; Score 33; DB 19; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDFV 6  
 1 111111  
 Db 1 grgdfv 6

RESULT 8

ID W41098 standard: Peptide; 6 AA.

AC W41098;

DT 08-JUN-1998 (first entry)

DE Alpha-v beta-3 antagonist cyclic peptide 62181.

KW Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;  
 KM vitronectin receptor; rheumatoid arthritis; tumour; metastasis;  
 KM diabetic retinopathy; macular degeneration; restenosis; therapy;  
 KM circular; cyclic.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 2 /note- "D-form residue"

FT W09745137-A1.

PN 04-DEC-1997.

PD 30-MAY-1997; 97MO-US09158.

PF 31-MAY-1996; 96US-0018733.

PR 31-MAY-1996; 96US-0015869.

PA (SCRI ) SCRIpps RES INST.

PI Brooks P, Cheresh DA;

DR WPI; 1998-032334/03.

PT Packaging material containing polypeptide antagonist of alphav,  
 PT beta3 integrin - used for inhibition of angiogenesis, and for  
 PT treating tumours, inflammation, eye diseases etc.

XX Example 1; Page 48; 234pp; English.

XX This synthetic RGD-containing cyclic peptide, designated 62181, is  
 CC a particularly preferred peptide that has integrin alpha-v beta-3  
 CC antagonist activity. It exhibits preferential inhibition of  
 CC fibronogen binding to the alpha v beta-3 receptor. It can be  
 CC prepared using standard solid-phase synthesis techniques (see  
 CC W41095-97). The invention relates to the discovery that  
 CC angiogenesis is mediated by the specific vitronectin receptor  
 CC alpha-v beta-3, and that inhibition of alpha-v beta-3 function  
 CC inhibits angiogenesis. Claimed antagonists of alpha-v beta-3  
 CC comprise C-terminal fragments (see W41083-94) of human or chicken  
 CC matrix metalloproteinase-2, fusion polypeptides, cyclic or linear  
 CC polypeptides, derivatised polypeptides, a monoclonal antibody or  
 CC organic mimetic compound. They can be used to inhibit angiogenesis  
 CC in inflamed tissue (for treatment of arthritis or rheumatoid  
 CC arthritis), in solid tumours or metastases (particularly to induce  
 CC regression or inhibit tumour growth), and in ocular disorders such  
 CC as diabetic retinopathy and macular degeneration, as well as to  
 CC treat restenosis (all claimed).

SQ Sequence 6 AA:

Query Match 100.0%; Score 33; DB 19; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDFV 6  
 1 111111  
 Db 1 grgdfv 6

RESULT 9

ID W41095 standard: Peptide; 6 AA.

AC W41095;

DT 08-JUN-1998 (first entry)

DE Alpha-v beta-3 antagonist precursor peptide.

KW Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;  
 KM vitronectin receptor; rheumatoid arthritis; tumour; metastasis;  
 KM diabetic retinopathy; macular degeneration; restenosis; therapy.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 1 /note- "N-terminus protected by Boc"

FT Misc-difference 2 /note- "D-form residue"

FT Modified-site 6 /note- "C-terminus protected by methyl ester"

FT W09745137-A1.

PN 04-DEC-1997.

PD 30-MAY-1997; 97MO-US09158.

PF 31-MAY-1996; 96US-0018733.

PR 31-MAY-1996; 96US-0015869.

PA (SCRI ) SCRIpps RES INST.

PI Brooks P, Cheresh DA;

DR WPI; 1998-032334/03.

PT Packaging material containing polypeptide antagonist of alphav,  
 PT beta3 integrin - used for inhibition of angiogenesis, and for  
 PT treating tumours, inflammation, eye diseases etc.

XX Example 1; Page 47; 234pp; English.

XX This synthetic RGD peptide was used in the preparation of a cyclic  
 CC peptide, designated 62181 (see W41098), that is an antagonist of  
 CC integrin alpha-v beta-3. The peptide was dissolved in methanol to  
 CC which 2 N NaOH solution was added. The admixture was stirred for 3  
 CC hr at 20 degC. After evaporation, the residue was taken up in  
 CC water, acidified to pH 3 with diluted HCl and extracted with ethyl  
 CC acetate. The peptide product (see W41096) was stirred at 20 degC  
 CC for 2 hr with 2 N HCl in dioxane to obtain a further peptide (see  
 CC W41097). This was treated with dicyclohexylcarbodiimide,  
 CC 1-hydroxybenzotriazole and N-methylmorpholine to produce peptide  
 CC 62181. The invention relates to the discovery that angiogenesis is  
 CC mediated by the specific vitronectin receptor alpha-v beta-3, and  
 CC that inhibition of alpha-v beta-3 function inhibits angiogenesis.  
 CC Claimed antagonists of alpha-v beta-3 comprise C-terminal fragments  
 CC (see W41083-94) of human or chicken matrix metalloproteinase-2,  
 CC fusion polypeptides, cyclic or linear polypeptides, derivatised

CC polypeptides, a monoclonal antibody or organic mimetic compound.  
XX  
SQ Sequence 6 AA:

Query Match 100.0%; Score 33; DB 19; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDFV 6  
Db 1 grgdfv 6

## RESULT 10

W41242  
ID W41242 standard; protein; 6 AA.

XX W41242;

DT 09-JUN-1998 (first entry)

DE Alpha-v-beta-5 antagonistic peptide 62181.

XX Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;  
KM angiogenesis; tumour growth; restenosis; neovascularisation.

XX Synthetic.

OS Key Location/Qualifiers

FT MISC-difference 1..6 "peptide is made cyclic via the first and  
FT last residues"

FT MISC-difference 2 /note="D-form residue"

PN W09745447-A1.

PD 04-DEC-1997.

PE 30-MAY-1997; 97NO-US09099.

PR 31-MAY-1996; 96US-0016733.

PR 31-MAY-1996; 96US-0015859.

PA (SCRI ) SCRIPPS RES INST.

PI Brooks P, Cheresch DA, Friedlander M;

DR WPI; 1998-041758/04.

PT Packaging material containing polypeptide antagonist of alphav,  
PT betas integrin - used for inhibition of angiogenesis, and for  
PT treating tumours, inflammation, eye diseases etc.

PS Disclosure; Page 41; 117pp; English.

XX The present peptide represents an alpha-v-beta-5 integrin antagonists.  
CC Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5  
CC can inhibit angiogenesis. The specification describes a novel  
CC labelled package that contains an inhibitor of angiogenesis i.e. an  
CC alpha-v-beta-5 antagonising polypeptide that binds to integrin  
CC alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.  
CC The antagonists are used to inhibit angiogenesis in inflamed tissue, in  
CC solid tumours or metastases, and in a wide range of ocular disorders  
CC (e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or  
CC corneal transplants). They are particularly used to induce regression or  
CC to inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be  
CC used to treat restenosis caused by migration of smooth muscle cells  
CC following angioplasty and to reduce blood supply to selected tissues.  
CC The antagonists particularly inhibit neovascularisation where this is  
CC induced by cytokines, e.g. transforming growth factor alpha, epidermal  
CC growth factor or especially vascular endothelial growth factor.

CC note: this sequence does not appear in the specification; it was created  
CC using information provided.  
XX

SQ Sequence 6 AA:

Query Match 100.0%; Score 33; DB 19; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDFV 6  
Db 1 grgdfv 6

## RESULT 11

R82393  
ID R82393 standard; peptide; 6 AA.

XX R82393;

DT 03-MAY-1996 (first entry)

DE Cyclic integrin alpha-v-beta-3 inhibitor peptide no. 62179.

XX Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;  
KM fibrinogen; inflammation; apoptosis; restenosis; cyclic.

XX Synthetic.

OS Key Location/Qualifiers

FT MISC-difference 2 /note="D-Ala"

PN W09525543-A1.

PD 28-SEP-1995.

PE 09-MAR-1995; 55WO-US03035.

PR 30-DEC-1994; 54US-0366655.

PR 18-MAR-1994; 94US-0210715.

PA (SCRI ) SCRIPPS RES INST.

PI Brooks P, Cheresch DA;

DR WPI; 1995-344463/44.

PT Inhibition of angiogenesis in a tissue, e.g. following angioplasty  
PT - by admin. of a compen. comprising an alpha-v-beta3 antagonist,  
PT useful for regression of established tumours, treating inflamed  
PT tissue, etc.

PS Example 1; Page 47; 135pp; English.

XX R82386-96 are a group of inhibitor peptides of integrin alpha-v-beta-3.  
CC The inhibitor peptides may be administered in a compen. and are useful  
CC for inhibition of inflamed tissue angiogenesis, e.g. that associated  
CC with rheumatoid arthritis, retinal angiogenesis associated with  
CC diabetic retinopathy, that associated with haemangioma, solid  
CC tumours, or solid tumour metastases. The alpha-v-beta-3 antagonists  
CC are also useful to induce apoptosis in neovascularisation in a tissue.  
CC The inhibitor peptides are pref. cyclic and contain an RGD sequence.

SQ Sequence 6 AA:

Query Match 90.9%; Score 30; DB 16; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.1e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDFV 6

Db 1 grgdf1 6

## RESULT 12

W41105 W41105 standard; Peptide; 6 AA.

AC W41105;

DT 08-JUN-1998 (first entry)

DE Cyclic peptide 62179.

XX Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;

KM vitronectin receptor; rheumatoid arthritis; tumour; metastasis;

KW diabetic retinopathy; macular degeneration; restenosis; therapy;

XX circular; cyclic.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 5 /note="D-form residue"

PN W09745137-A1.

PD 04-DEC-1997.

PF 30-MAY-1997; 97WO-US09158.

XX 31-MAY-1996; 96US-0013733.

PR 31-MAY-1996; 96US-0013689.

XX (SCRI ) SCRIPPS RES INST.

PI Brooks P, Cheresch DA;

XX WPI; 1998-032334/03.

DR Packaging material containing polypeptide antagonist of alpha-v

PT beta3 integrin - used for inhibition of angiogenesis, and for

XX treating tumours, inflammation, eye diseases etc.

PS Example 1; Page 51; 234pp; English.

XX This synthetic cyclic peptide, designated 62179, was examined as

CC a potential antagonist of integrin alpha-v beta-3. It was

CC prepared using standard solid-phase synthesis techniques. Unlike

CC RGD-containing or RGD-derivatised cyclic peptides (see W41098-101),

CC peptide 62179 did not exhibit preferential inhibition of fibrinogen

CC binding to the alpha-v beta-3 receptor. The invention relates to

CC the discovery that angiogenesis is mediated by the specific

CC vitronectin receptor alpha-v beta-3, and that inhibition of alpha-v

CC beta-3 function inhibits angiogenesis. Claimed antagonists of

CC alpha-v beta-3 comprise C-terminal fragments (see W41083-94) of

CC human or chicken matrix metalloproteinase-2, fusion polypeptides,

CC cyclic or linear polypeptides, derivatised polypeptides, a

CC monoclonal antibody or organic mimetic compound.

R11760  
ID R11760 standard; Protein; 5 AA.  
XX R11760;  
AC R11760;  
DT 03-JUL-1991 (first entry)  
XX Peptide #4 having cell recognition sequence.  
DE Cell surface adhesion; receptor mediated attachment; culture;  
XX substrate.  
KM Synthetic.  
OS Synthetic.  
XX W09105036-A.  
PN 18-APR-1991.  
PD 27-SEP-1990; 30WO-US05525.  
PF 28-SEP-1989; 89US-041414.  
PR 21-MAY-1990; 30US-0527198.  
XX (TEXA ) UNIV OF TEXAS SYST.  
XX Hubbell JA, Nassia SP, Desai NP;  
PI WPI; 1991-132844/18.  
DR Surfaces having cell adhesive effects - formed by covalently linking  
XX small peptides which facilitate cell receptor mediated attachment of  
PT cells.  
PS Claim 3; Page 91; 127pp; English.  
XX The peptide, and shorter versions eg RGD, including the cell  
CC recognition sequence RGD, can be used to prepare a cell culture  
CC substrate. A surface (glass, PET etc) is chemically derivatised  
CC with the peptides to yield a proteolytically stable, reusable  
CC surface which promotes the amt. of and enhances the rate of receptor  
CC mediated cell adhesion. See also R11757-R11762.  
XX Sequence 5 AA;  
SQ

Query Match 87.9%; Score 29; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDF 5  
Db 1 grgdf 5

## RESULT 14

R24515 R24515 standard; Protein; 5 AA.

AC R24515;

DT 02-DEC-1992 (first entry)

DE Platelet antagonist peptide 2.

XX Clinical effect; antagonist.

OS Synthetic.

XX JP04134096-A.

PN 07-MAY-1992.

PF 21-SEP-1990; 90JP-0253849.

RESULT 13

Query Match 90.9%; Score 30; DB 19; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.1e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDFV 6  
Db 1 grgdf1 6

XX 21-SEP-1990; 90JP-0253849.  
 XX (SEGR ) SEIKAGAKU KOGYO CO LTD.  
 XX WPI; 1992-204525/25.  
 XX New peptide(s) comprising arginine-glycine-asparagine and  
 PT hyaluronic acid - useful as platelet antagonists with higher  
 PT activity than arginine-glycine-asparagine-valine  
 XX Disclosure; Page 5; 10pp; Japanese.  
 XX The sequences given in R24514-8 are peptides which are useful as  
 CC platelet antagonists. These peptides have higher activity than the  
 CC conventional peptide of Arg-Gly-Asp-Val. These peptides have a  
 CC clinical effect at a lower dose, dosage is 2.5-5.0 mg/kg/day.  
 XX Sequence 5 AA:  
 SQ

Query Match 87.9%; Score 29; DB 13; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDF 5  
 |||||  
 Db 1 grgdf 5

## RESULT 15

R69327 ID R69327 standard; peptide; 6 AA.

XX AC R69327;

XX DT 25-JUN-1995 (first entry)

XX DE Gp IIb/IIIa receptor ligand used in scintigraphic imaging of thrombi.

XX KW Scintigraphy; thrombus; thrombi; imaging; specific binding;

XX KM technetium-99m; radiolabelled; Gp IIb/IIIa receptor ligand.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note="(S-benzoyl-2-mercaptoacetyl)-Gly"

XX WO93323085-A.

XX PD 25-NOV-1993.

XX PF 21-MAY-1993; 93WO-US04794.

XX PR 21-MAY-1992; 92US-0886752.

XX PA (DIAT-) DIATECH INC.

XX PI Dean RT, Lister-James T;

XX DR WPI; 1993-386229/48.

XX PT Reagent for scintigraphic imaging of thrombi with 99m technetium

PT - comprises synthetic peptide which binds to thrombus, covalently

PT coupled to metal binding gp.; rapidly cleared from blood and

XX PS tissue

XX Claim 41; Page 46; 61pp; English.

CC The invention relates to reagents for scintigraphic imaging of a

CC thrombus in-vivo, comprising (A) a specific binding compound capable of

CC binding to at least one component of a thrombus, covalently linked

CC to (B) a technetium-99m-binding moiety. Specific peptides

CC constituting the reagents are claimed as new. The present peptide is

CC one such peptide.

XX SQ Sequence 5 AA:

Query Match 87.9%; Score 29; DB 14; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDF 5  
 |||||  
 Db 2 grgdf 5

Search completed: March 6, 2001, 09:42:54  
 Job time: 37 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 6, 2001, 09:42:18 ; Search time 12.64 Seconds

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Title: US-09-081-522-4

Perfect score: 33

Sequence: 1 GRGDFV 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 23537

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	33	100.0	6	1	US-08-366-665-2
7	33	100.0	6	1	US-08-366-665-3
8	33	100.0	6	1	US-08-366-665-4
9	30	90.9	6	1	US-08-210-715-11
10	30	90.9	6	1	US-08-366-665-11
11	29	87.9	5	5	5330911-13
12	29	87.9	6	1	US-08-482-880-21
13	29	87.9	6	1	US-08-482-880-25
14	29	87.9	6	2	US-08-213-274-21
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23	29	87.9	6	2	US-08-361-864-25
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30	26	78.8	5	5	5330911-3	Patent No. 5330911
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36	23	69.7	4	1	US-08-461-611-36	Sequence 12, Appl1
37	23	69.7	4	1	US-08-596-116A-68	Sequence 12, Appl1
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#### ALIGNMENTS

RESULT 1  
US-08-210-715-1  
Sequence 1, Application US/08210715  
Patent No. 5753230  
GENERAL INFORMATION:  
APPLICANT: Brooks, Peter  
APPLICANT: Chetesh, David A  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
INHIBITION OF ANGIOGENESIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Office of Patent Counsel, The Scripps  
ADDRESSER: Research Institute  
STREET: 10665 NO. 5753230th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/210,715  
FILING DATE: 18-MAR-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 419.0  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
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OTHER INFORMATION: /note- "BOC signifies the N-terminal protecting  
OTHER INFORMATION: group butyloxycarbonyl; Ome signifies a C-terminal  
OTHER INFORMATION: methyl ester; arginine in the second position

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OTHER INFORMATION: /note="A prefix "D" in D-Arg signifies that the
OTHER INFORMATION: arginine in position 2 is a D-amino acid."
US-08-210-715-1

Query Match      100.0%; Score 33; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRGDFV 6
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Db       1 GRGDFV 6

RESULT      2
US-08-210-715-2
Sequence 2, Application US/08210715
Patent No. 5753230
GENERAL INFORMATION:
APPLICANT: Brooks, Peter
APPLICANT: Cheres, David A
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 No. 5753230th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/210,715
FILING DATE: 18-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 419.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
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OTHER INFORMATION: /note="BOC signifies the N-terminal blocking
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NAME/KEY: Peptide
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OTHER INFORMATION: /note="A prefix "D" in D-Arg signifies that the
OTHER INFORMATION: arginine in position 2 is a D-amino acid."
US-08-210-715-2

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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRGDFV 6
        |||||
Db       1 GRGDFV 6

RESULT      3
US-08-210-715-3
Sequence 3, Application US/08210715
Patent No. 5753230
GENERAL INFORMATION:
APPLICANT: Brooks, Peter
APPLICANT: Cheres, David A
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 No. 5753230th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: CA
COUNTRY: USA
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/210,715
FILING DATE: 18-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 419.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..6
OTHER INFORMATION: /label=H
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OTHER INFORMATION: /note= "H signifies a free N-terminal amine."  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
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NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /note= "A prefix "D" in D-Arg at position 2,"  
OTHER INFORMATION: signifies that the arginine is a D-amino acid."  
US-08-210-715-3

Query Match 100.0%; Score 33; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDFV 6  
Db 1 GRGDFV 6

RESULT 4  
US-08-210-715-4  
Sequence 4, Application US/08210715  
Patent No. 5753230  
GENERAL INFORMATION:  
APPLICANT: Brooks, Peter  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESS: Research Institute  
STREET: 10666 No. 5753230th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/210,715  
FILING DATE: 18-MAR-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 419.0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /label= cyclo

OTHER INFORMATION: /note= "Cyclo signifies a cyclic peptide; lower  
OTHER INFORMATION: case letters indicate a D-amino acid; capital  
OTHER INFORMATION: letters indicate a L-amino acid."  
US-08-210-715-4

Query Match 100.0%; Score 33; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDFV 6  
Db 1 GRGDFV 5

RESULT 5  
US-08-366-665-1  
Sequence 1, Application US/08366665  
Patent No. 5766591  
GENERAL INFORMATION:  
APPLICANT: Brooks, Peter  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESS: Research Institute  
STREET: 10665 No. 5766591th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/366,665  
FILING DATE: 30-DEC-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/210,715  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 419.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /label= BOC-GRGDFV-OMe  
OTHER INFORMATION: /note= "BOC signifies the N-terminal protecting  
OTHER INFORMATION: group butyloxycarbonyl; OMe signifies a C-terminal  
OTHER INFORMATION: methyl ester; arginine in the second position  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /label= OMe

OTHER INFORMATION: /note="Ome signifies the C-terminal protecting  
OTHER INFORMATION: group methyl ester."  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /label-D-Arg  
OTHER INFORMATION: /note="A prefix "D" in D-Arg signifies that the  
OTHER INFORMATION: arginine in position 2 is a D-amino acid."  
US-08-366-665-1

Query Match 100.0%; Score 33; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GRGDFV 6  
DB 1 GRGDFV 6

RESULT 6  
US-08-366-665-2  
Sequence 2, Application US/08366665  
Patent No. 5766591  
GENERAL INFORMATION:  
APPLICANT: Brooks, Peter  
APPLICANT: Cheres, David A  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 No. 5766591th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/366,665  
FILING DATE: 30-DEC-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/210,715  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Filling, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 419.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /label-BOC  
OTHER INFORMATION: /note="BOC signifies the N-terminal blocking  
OTHER INFORMATION: group tertbutyloxycarbonyl."

FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /label-OH  
OTHER INFORMATION: /note="OH signifies a free C-terminal carboxylic  
OTHER INFORMATION: acid."  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /label-D-Arg  
OTHER INFORMATION: /note="A prefix "D" in D-Arg signifies that the  
OTHER INFORMATION: arginine in position 2 is a D-amino acid."  
US-08-366-665-2

Query Match 100.0%; Score 33; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GRGDFV 6  
DB 1 GRGDFV 6

RESULT 7  
US-08-366-665-3  
Sequence 3, Application US/08366665  
Patent No. 5766591  
GENERAL INFORMATION:  
APPLICANT: Brooks, Peter  
APPLICANT: Cheres, David A  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 No. 5766591th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/366,665  
FILING DATE: 30-DEC-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/210,715  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Filling, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 419.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Peptide

LOCATION: 1..6 /label- H  
OTHER INFORMATION: /note- "H signifies a free N-terminal amine."  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /label- OH  
OTHER INFORMATION: /note- "OH signifies a free C-terminal carboxylic  
OTHER INFORMATION: acid."  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /label- D-Arg  
OTHER INFORMATION: /note- "A prefix "D" in D-Arg at position 2,  
OTHER INFORMATION: signifies that the arginine is a D-amino acid."  
US-08-366-665-3

Query Match 100.0%; Score 33; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDFV 6  
DB 1 GRGDFV 6

RESULT 8  
US-08-366-665-4  
Sequence 4, Application US/08366665  
Patent No. 5766591  
GENERAL INFORMATION:  
APPLICANT: Brooks, Peter  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
NUMBER OF INVENTION: INHIBITION OF ANGIOGENESIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESS: Research Institute  
STREET: 10665 No. 5766591th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/366,665  
FILING DATE: 30-DEC-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/210,715  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 419.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

FRAGMENT TYPE: Internal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /label- cyclo  
OTHER INFORMATION: /note- "Cyclo signifies a cyclic peptide; lower  
OTHER INFORMATION: case letters indicate a D-amino acid; capital  
OTHER INFORMATION: letters indicate a L-amino acid."  
US-08-366-665-4

Query Match 100.0%; Score 33; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDFV 6  
DB 1 GRGDFV 6

RESULT 9  
US-08-210-715-11  
Sequence 11, Application US/08210715  
Patent No. 5753230  
GENERAL INFORMATION:  
APPLICANT: Brooks, Peter  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
NUMBER OF INVENTION: INHIBITION OF ANGIOGENESIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESS: Research Institute  
STREET: 10665 No. 5753230th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/210,715  
FILING DATE: 18-MAR-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 419.0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /label- cyclo  
OTHER INFORMATION: /note- "Cyclo signifies a cyclic peptide; lower  
OTHER INFORMATION: case letters indicate a D-amino acid; capital  
OTHER INFORMATION: letters indicate a L-amino acid."  
US-08-210-715-11

Query Match 90.9%; Score 30; DB 1; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1.3e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GRGDFV 6  
|||||:  
Db 1 GRGDFL 6

RESULT 10  
US-08-366-665-11  
; Sequence 11, Application US/08366665  
; Patent No. 5766591  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; APPLICANT: Cheres, David A  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
; TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Office of Patent Counsel, The Scripps  
; STREET: 10666 No. 576591th Torrey Pines Road, TPC-8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/366,665  
; FILING DATE: 30-DEC-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/210,715  
; FILING DATE: 18-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: TSRI 419.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 554-2937  
; TELEFAX: (619) 554-6312  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: circular  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..6  
; OTHER INFORMATION: /label= cyclo  
; OTHER INFORMATION: /note= "Cyclo signifies a cyclic peptide; lower  
; OTHER INFORMATION: case letters indicate a D-amino acid; capital  
; OTHER INFORMATION: letters indicate a L-amino acid."  
US-08-366-665-11

Query Match 90.9%; Score 30; DB 1; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1.3e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GRGDFV 6  
|||||:

Db 1 GRGDFL 6

RESULT 11  
5330911-13  
; Patent No. 5330911  
; APPLICANT: HUBBELL, JEFFREY A.; MASSIA, STEPHEN P.; DESAI,  
; NEIL P.  
; TITLE OF INVENTION: SURFACES HAVING DESIRABLE CELL  
; ADHESIVE EFFECTS  
; NUMBER OF SEQUENCES: 27  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/527,198  
; FILING DATE: 21-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 414,144  
; FILING DATE: 28-SEP-1989  
; SEQ ID NO: 13:  
; LENGTH: 5  
5330911-13

Query Match 87.9%; Score 29; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GRGDF 5  
|||||:  
Db 1 GRGDF 5

RESULT 12  
US-08-482-880-21  
; Sequence 21, Application US/08482880  
; Patent No. 5736122  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Richard T  
; APPLICANT: Lister-James, John  
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
; TITLE OF INVENTION: Thrombus Imaging  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Allegretti, Ltd.  
; STREET: 10 South Wacker Drive Suite 3000  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/482,880  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: NO. 5736122nan, Kevin E  
; REGISTRATION NUMBER: 35,303  
; REFERENCE/DOCKET NUMBER: 92,216-L  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-715-1000  
; TELEFAX: 312-715-1234  
; TELEX: 910-221-5317  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-482-880-21

Query Match 87.9%; Score 29; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 GRGDF 5  
Db 2 GRGDF 6

## RESULT 13

US-08-482-880-25  
Sequence 25, Application US/08482880  
Patent No. 5736122

## GENERAL INFORMATION:

APPLICANT: Dean, Richard T  
TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Allegretti, Ltd.  
STREET: 10 South Wacker Drive Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,880  
FILING DATE: 07-JUN-1995

## CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: No. 5736122nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,216-L  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317

## INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-880-25

Query Match 87.9%; Score 29; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 GRGDF 5  
Db 2 GRGDF 6

## RESULT 14

US-08-273-274-21  
Sequence 21, Application US/08273274  
Patent No. 5849260

## GENERAL INFORMATION:

APPLICANT: Dean, Richard T  
TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Allegretti & Witcoff, Ltd.  
STREET: 10 South Wacker Drive Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60605

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/273,274  
FILING DATE:

## CLASSIFICATION: 436

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/886,752  
FILING DATE: 21-MAY-1992

## ATTORNEY/AGENT INFORMATION:

NAME: No. 5849260nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,216  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317

## INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-273-274-21

Query Match 87.9%; Score 29; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 GRGDF 5  
Db 2 GRGDF 6

## RESULT 15

US-08-273-274-25  
Sequence 25, Application US/08273274  
Patent No. 5849260

## GENERAL INFORMATION:

APPLICANT: Dean, Richard T  
TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Allegretti & Witcoff, Ltd.  
STREET: 10 South Wacker Drive Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/273,274  
FILING DATE:  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/886,752  
FILING DATE: 21-MAY-1992

ATTORNEY/AGENT INFORMATION:  
NAME: No. 5849260nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,216  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-273-274-25

Query Match 87.9%; Score 29; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 1 GRGDF 5  
|||||  
Db 2 GRGDF 6

Search completed: March 6, 2001, 09:42:36  
Job time: 18 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 6, 2001, 09:42:22 ; Search time 13.62 Seconds

(Without alignments)  
29.912 Million cell updates/sec

Title: US-09-081-522-4

Perfect score: 33  
Sequence: 1 GRGDFV 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 315

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR-66:\*\*  
1: pirl:\*\*  
2: pirl2:\*\*  
3: pirl3:\*\*  
4: pirl4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	51.5	5	2 PT0608	T-cell receptor be
2	17	51.5	6	2 IS1434	H4 histone - Afric
3	13	39.4	6	2 PT0629	T-cell receptor be
4	13	39.4	6	2 PT0514	T-cell receptor be
5	13	39.4	6	2 A43129	neuropeptide GnFR
6	12	36.4	4	2 PT0711	T-cell receptor be
7	12	36.4	5	2 A32516	cholecystokinin-5
8	12	36.4	5	2 PQ0689	photosystem I 10.4
9	12	36.4	5	2 A44692	fullin - giant At
10	12	36.4	5	2 B61445	Leu-enkephalin - b
11	12	36.4	5	2 A61445	Met-enkephalin - b
12	12	36.4	5	2 PT0513	T-cell receptor be
13	12	36.4	5	2 PT0538	T-cell receptor be
14	12	36.4	5	2 PT0703	T-cell receptor be
15	12	36.4	5	2 PT0690	T-cell receptor be
16	12	36.4	5	2 PT0573	T-cell receptor be
17	12	36.4	5	2 PT0679	T-cell receptor be
18	12	36.4	6	2 PT0511	T-cell receptor be
19	12	36.4	6	2 PT0604	T-cell receptor be
20	12	36.4	6	2 PT0630	T-cell receptor be
21	12	36.4	6	2 PT0687	T-cell receptor be
22	12	36.4	6	2 PT0652	T-cell receptor be
23	12	36.4	6	2 PT0587	T-cell receptor be
24	12	36.4	6	2 PT0568	T-cell receptor be
25	12	36.4	6	2 PT0709	T-cell receptor be
26	12	36.4	6	2 PD0028	pev-kinin 2 - pen
27	11	33.3	4	1 ECXNA	antho-NF amide neur
28	11	33.3	4	2 A25844	myosin-11gt-chain
29	11	33.3	4	2 S39390	

30	11	33.3	4	2 S47552	ubiquitin - rat
31	11	33.3	5	2 C23751	spinal cord peptid
32	11	33.3	5	2 I40702	primase - Citrobac
33	11	33.3	5	2 B61168	cocoonase (Ec 3.4.
34	11	33.3	5	2 S53595	hypothetical prote
35	11	33.3	5	2 D44823	synaptosomal-assoc
36	11	33.3	5	2 C53284	T-cell receptor be
37	11	33.3	5	2 PT0525	T-cell receptor be
38	11	33.3	5	2 PT0553	T-cell receptor be
39	11	33.3	5	2 PT0695	T-cell receptor be
40	11	33.3	5	2 PT0700	T-cell receptor be
41	11	33.3	6	2 A60494	antileoplastic gly
42	11	33.3	6	2 PT0280	ig heavy chain CRU
43	11	33.3	6	2 PT0605	T-cell receptor be
44	11	33.3	6	2 PT0641	T-cell receptor be
45	11	33.3	6	2 PT0668	T-cell receptor be

#### ALIGNMENTS

RESULT 1  
PT0608  
T-cell receptor beta chain V-D-J region (120-206) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #ext\_change 30-May-1997  
C:Accession: PT0608  
R:Feeney, A.J.  
U. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
A:Reference number: PT0509; MID:91277601  
A:Accession: PT0608  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <PEP>  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 51.5%; Score 17; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRG 3  
DB 3 GRG 5

RESULT 2  
IS1434  
H4 histone - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #ext\_change 21-Jul-2000  
C:Accession: IS1434  
R:Woodland, H.R.; Warrington, J.R.; Ballantine, J.E.M.; Turner, P.C.  
Nucleic Acids Res. 12, 4939-4958, 1984  
A:Title: Are there major developmentally regulated H4 gene classes in Xenopus?  
A:Reference number: IS1391; MID:84247348  
A:Accession: IS1434  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-6 <MOO>  
A:Cross-references: GB:K02304; NID:g214227; PIDN:AAA9738.1; PID:g555517

Query Match 51.5%; Score 17; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRG 3  
DB 3 GRG 5

RESULT 3  
PT0629  
T-cell receptor beta chain V-D-J region (100-2AH) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0629; PT0528  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0629  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FE2>  
A:Experimental source: newborn thymus, strain BALB/c, clone 100-2AH  
A:Accession: PT0528  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FE2>  
A:Experimental source: adult thymus, strain BALB/c, clone 100-4AB  
C:Keywords: T-cell receptor

Query Match 39.4%; Score 13; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 GDF 5  
1:1  
Db 3 GDW 5

RESULT 4  
PT0514  
T-cell receptor beta chain V-D-J region (100-4AC) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0514  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0514  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FE2>  
A:Experimental source: adult thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 39.4%; Score 13; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GRG 3  
1:1  
Db 4 GOG 6

RESULT 5  
A43129  
neuropeptide GnFRFRamide - tapeworm (Moniezia expansa)  
C:Species: Moniezia expansa  
C>Date: 10-Nov-1997 #sequence\_revision 14-Nov-1997 #text\_change 14-Nov-1997  
C:Accession: A43129  
R:Kaul, A.; Shaw, C.; Halton, D.; Thim, L.  
Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993  
A:Title: GnFRFRamide: A novel FMRFamide-immunoreactive peptide isolated from the sheep  
A:Reference number: A43129; MUID:93312289  
A:Accession: A43129  
A:Molecule type: protein  
A:Residues: 1-6 <MAU>

C:Keywords: amidated carboxyl end; neuropeptide  
F:6/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 39.4%; Score 13; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 GDF 5  
1:1  
Db 1 GNF 3

RESULT 6  
PT0711  
T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0607; PT0674; PT0570; PT0711; PT0710  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0607  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-4 <FE2>  
A:Experimental source: newborn thymus, strain BALB/c, 120-2J  
A:Accession: PT0674  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-4 <FE2>  
A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G  
A:Accession: PT0678  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-4 <FE2>  
A:Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I  
A:Accession: PT0711  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-4 <FE5>  
A:Experimental source: newborn thymus, strain BALB/c (clones 161-2AF and 161-2AF)  
C:Keywords: T-cell receptor

Query Match 36.4%; Score 12; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GD 4  
1:1  
Db 3 GD 4

RESULT 7  
A32516  
cholecystokinin-5 - dog  
N:Alternate names: CCK-5  
C:Species: Canis lupus familiaris (dog)  
C>Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 18-Aug-2000  
C:Accession: A32516  
R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.  
Am. J. Physiol. 252, G272-G275, 1987  
A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in  
A:Reference number: A32516; MUID:87153871  
A:Accession: A32516  
A:Molecule type: protein



A:Residues: 1-5 <SHI>  
C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecyst  
C:Superfamily: gastrin  
C:Keywords: amidated carboxyl end; neuropeptide  
F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 36.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DF 5  
||  
DB 4 DF 5

RESULT 8  
P00689  
Photosystem I 10.4K H1 chain - common tobacco (fragment)  
C:Species: Nicotiana tabacum (common tobacco)  
C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
C:Accession: P00689  
R:Okada, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.  
Plant Physiol. 102, 1259-1267, 1993  
A:Title: Molecular heterogeneity of photosystem I. psad, psae, psaf, psah and psal are  
A:Reference number: P00687; MUID:94105345  
A:Accession: P00689  
A:Molecule type: protein  
A:Residues: 1-5 <OBO>  
C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 36.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GD 4  
||  
DB 3 GD 4

RESULT 9  
A44692  
Fulicin - giant African snail  
C:Species: Achatina fulica (giant African snail)  
C:Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 11-Jul-1997  
C:Accession: A44692  
R:Ohla, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, R.; No  
Biochem. Biophys. Res. Commun. 178, 486-493, 1991  
A:Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from t  
A:Reference number: A44692; MUID:91315471  
A:Accession: A44692  
A:Molecule type: protein  
A:Residues: 1-5 <OHT>  
C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide  
F:2/Modified site: D-asparagine (Asn) #status experimental  
F:5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 36.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 DFV 6  
||  
DB 3 DFV 5

RESULT 10  
B61445  
Leu-enkephalin - blue mussel  
C:Species: Mytilus edulis (blue mussel)  
C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000

C:Accession: B61445  
R:Leung, M.K.; Stefano, G.B.  
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul  
A:Reference number: A61445; MUID:84144823  
A:Accession: B61445  
A:Molecule type: protein  
A:Residues: 1-5 <LEU>  
A:Experimental source: pedal ganglia  
C:Keywords: neuropeptide; opioid peptide

Query Match 36.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 GDFV 6  
||  
DB 2 GGFL 5

RESULT 11  
A61445  
Met-enkephalin - blue mussel  
C:Species: Mytilus edulis (blue mussel)  
C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000  
C:Accession: A61445  
R:Leung, M.K.; Stefano, G.B.  
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul  
A:Reference number: A61445; MUID:84144823  
A:Accession: A61445  
A:Molecule type: protein  
A:Residues: 1-5 <LEU>  
A:Experimental source: pedal ganglia  
C:Keywords: neuropeptide; opioid peptide

Query Match 36.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 GDFV 6  
||  
DB 2 GGFM 5

RESULT 12  
PT0513  
T-cell receptor beta chain V-D-J region (100-4AL) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0513; PT0606  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Functional sequences of fetal T cell receptor beta chains have few N regions  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0513  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <EE>  
A:Experimental source: adult thymus, strain BALB/c, clone 100-4AL  
A:Accession: PT0606  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: newborn thymus, strain BALB/c, clone 120-15  
C:Keywords: T-cell receptor

Query Match 36.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GD 4  
||  
Db 3 GD 4

## RESULT 13

PT0538  
T-cell receptor beta chain V-D-J region (126-1F) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0538; PT0539; PT0603  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0538  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F  
A:Accession: PT0539  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE3>  
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F  
A:Accession: PT0603  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: newborn thymus, strain BALB/c, clone 100-2AC  
C:Keywords: T-cell receptor

Query Match 36.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GD 4  
||  
Db 3 GD 4

## RESULT 14

PT0703  
T-cell receptor beta chain V-D-J region (135-1F) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0703  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0703  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 36.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GD 4  
||  
Db 3 GD 4

## RESULT 15

PT0690  
T-cell receptor beta chain V-D-J region (140-1BD) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0690  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0690  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: day 18 fetal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 36.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GD 4  
||  
Db 3 GD 4

Search completed: March 6, 2001, 09:43:11  
Job time: 49 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 6, 2001, 09:42:41 ; Search time 8.47 Seconds

(without alignments)  
22.877 Million cell updates/sec

Title: US-09-081-522-4

Perfect score: 33  
Sequence: 1 GRGDEV 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 38

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_33.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	39.4	6	1 FARP_MONEX	P41966 moniezia ex
2	12	36.4	5	1 UXA4_CHLTR	P38005 chlamydia t
3	11	33.3	5	1 UF01_MOUSE	P38639 mus musculu
4	10	30.3	5	1 TPIS_CANEA	P54719 canis famli
5	10	30.3	6	1 CIP1_MYTE	P13736 mytilus edu
6	10	30.3	6	1 CIP2_MYTE	P13737 mytilus edu
7	9	27.3	4	1 ACH1_ACHFU	P35904 achatina fu
8	9	27.3	5	1 PAP2_PAPMA	P81864 pardachirus
9	8	24.2	4	1 TRM3_ECOLI	P13973 escherichia
10	7	21.2	4	1 FLRF_HIRME	P42561 hirudo medi
11	7	21.2	4	1 FMRF_MACNI	P01162 macrocallis
12	6	18.2	3	1 GRM4_HUMAN	P01167 homo sapien
13	6	18.2	3	1 LUXE_VIBET	P24272 vibrio fisc
14	6	18.2	4	1 DCML_PSECH	P19916 pseudomonas
15	6	18.2	4	1 EOS1_HUMAN	P02731 homo sapien
16	6	18.2	4	1 FARS_HIRME	P42562 hirudo medi
17	6	18.2	4	1 FARA_HIRME	P42563 hirudo medi
18	6	18.2	5	1 ALI4_CARMA	P81817 carcinus ma
19	6	18.2	5	1 BIOC_CITER	P13071 citrobacter
20	6	18.2	5	1 BIOR_SALTY	P12677 salmonella
21	6	18.2	5	1 FARP_ARTTR	P11853 artipocsthi
22	6	18.2	5	1 SUGA_ACHDO	P19991 acheta dome
23	6	18.2	5	1 UC22_MAIZE	P80638 zea mays (m
24	6	18.2	6	1 LOK1_LOCTI	P41451 locusta mig
25	6	18.2	4	1 TRP1_PSEPU	P36414 pseudomonas
26	6	15.2	4	1 TRP1_HUMAN	P01858 homo sapien
27	5	15.2	5	1 BIOR_SALTY	P12678 salmonella
28	5	15.2	5	1 PRC1_PERAM	P01373 periplaneta
29	5	15.2	4	1 ACPH_RABIT	P25154 cryptolagus
30	4	12.1	4	1 RM01_YEAST	P36515 saccharomyc
31	3	9.1	6	1 OVM_HERPE	P42965 leptinotars
32	3	9.1	6	1 UN06_CLOPA	P81351 clostridium
33	2	6.1	4	1 DCMS_PSECH	P19918 pseudomonas

34	2	6.1	5	1 BPP7_BOTIN	P30425 bothrops in
35	2	6.1	6	1 VP19_HSVIK	P23210 herpes simp
36	1	3.0	3	1 THYL_PIG	P01151 sus scrofa
37	1	3.0	5	1 BIOC_CITER	P12997 citrobacter
38	1	3.0	6	1 TMOF_SARBU	P41495 sarcophaga

## ALIGNMENTS

RESULT	1	STANDARD	PRT	6 AA
FARP_MONEX				
ID	FARP_MONEX			
AC	P41966			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	FMRFAMIDE-LIKE NEUROPEPTIDE GNEFRF-AMIDE.			
OS	Moniezia expansa (Sheep tapeworm).			
OC	Eukaryota; Metazoa; Platyhelminthes; Neodermata; Cestoda; Eucestoda; Cyclophyllidae; Anoplocephalidae; Moniezia.			
CC	[1]			
RP	SEQUENCE.			
RX	MEDLINE-9331289; Pubmed-8323531;			
RA	Maule A.G., Shaw C., Halton D.W., Thim L.;			
RT	"GNEFRFamide: a novel FMRFamide-immunoreactive peptide isolated from the sheep tapeworm, Moniezia expansa".			
RL	Biochem Biophys Res Commun. 193:1054-1060(1993).			
CC	-1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.			
KW	Neuropeptide; Amidation.			
FT	MOD RES 6			
SO	SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;			

Query Match 39.4%; Score 13; DB 1; Length 6;  
Best Local Similarity 66.7%; Pred. No. 8.9e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT	2	STANDARD	PRT	5 AA
UXA4_CHLTR				
ID	UXA4_CHLTR			
AC	P38005			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	01-OCT-1994 (Rel. 30, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).			
OS	Chlamydia trachomatis.			
OC	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.			
CC	[1]			
RP	SEQUENCE.			
RC	SRRAIN-L2/434/BU;			
RA	Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,			
RA	Comanducci M., Christensen G., Birkelund S., Vreton E., Ratti G.,			
RA	Pallini V.;			
RL	Submitted (SEP-1994) to the SWISS-PROT data bank.			
CC	-1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN			
CC	PROTEIN IS: 4.5, ITS MW IS: 28 KDA.			
FT	NON-TER 5			
SO	SEQUENCE 5 AA; 474 MW; 75BA865A800000 CRC64;			

Query Match 36.4%; Score 12; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GD 4  
11

Db 3 GD 4

RESULT 3  
UF01\_MOUSE STANDARD; PRT; 5 AA.

AC P38639;  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DE 01-FEB-1995 (Rel. 31, Last annotation update)  
DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP TISSUE-FIBROBLAST;  
RC MEDLINE-95009907; PubMed-7523103;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins  
using preparative two-dimensional gel electrophoresis.";  
RT Electrophoresis 15:735-745(1994)  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
FT PROTEIN IS: 6.6, ITS MW IS: 19 KDA.  
SO NON\_TER 5  
SEQUENCE 5 AA: 717 MW; 7364087043100000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GR 2  
DB 3 GR 4

RESULT 4

TPIS\_CANFA STANDARD; PRT; 5 AA.

AC P34714;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE TRIOSPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).  
GN Tpi1.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
NC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
RN [1]  
RP TISSUE-HEART;  
RC MEDLINE-98163340; PubMed-9504812;  
RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
dog heart proteins.";  
RT Electrophoresis 18:2795-2802(1997).  
CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE = DIHYDROXY-  
ACETONE PHOSPHATE.  
CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE TRIOSPHOSPHATE ISOMERASE FAMILY.  
DR HSC-2DPAGE; P54714; DOG.  
DR INTERPRO: IPR000652; -.  
DR PROSITE: PS001771; TIM; PARTIAL.  
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;  
FT NON\_TER 1  
FT MOD\_RES 5  
SEQUENCE 5 AA: 550 MW; 64444862C9A00000 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FV 6  
DB 1 FV 2

RESULT 5

CIP2\_MYTED STANDARD; PRT; 6 AA.

AC P13736;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE CONTRACTION-INHIBITING PEPTIDE I (MIP I).  
OS Mytilus edulis (Blue mussel).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
NC Mytiloidea; Mytilidae; Mytilus.  
RN [1]  
RP TISSUE-PEDAL GANGLION;  
RC MEDLINE-88240357; PubMed-3377776;  
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;  
RT "Structures and actions of Mytilus inhibitory peptides.";  
RT Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
CC -1- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN  
MUSCLES.  
CC -1- SIMILARITY: TO MIP II.  
DR PIR; A27696; A27696.  
KW Hormone; Amidation.  
FT MOD\_RES 6  
SEQUENCE 6 AA: 637 MW; 72C9C68775B81000 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FV 6  
DB 5 FV 6

RESULT 6

CIP2\_MYTED STANDARD; PRT; 6 AA.

AC P13737;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE CONTRACTION-INHIBITING PEPTIDE II (MIP II).  
OS Mytilus edulis (Blue mussel).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
NC Mytiloidea; Mytilidae; Mytilus.  
RN [1]  
RP TISSUE-PEDAL GANGLION;  
RC MEDLINE-88240357; PubMed-3377776;  
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;  
RT "Structures and actions of Mytilus inhibitory peptides.";  
RT Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
CC -1- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN  
MUSCLES.  
CC -1- SIMILARITY: TO MIP I.  
DR PIR; B27696; B27696.  
KW Hormone; Amidation.  
FT MOD\_RES 6  
SEQUENCE 6 AA: 621 MW; 72C9C6876D81000 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FV 6  
11  
Db 5 FV 6

RESULT 7  
ACHL\_ACHFU STANDARD; PRT; 4 AA.  
ID ACHL\_ACHFU  
AC P35904;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE ACHATIN-I.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Achatinacea; Achatinidae; Achatina.  
RN [1]  
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.  
RC STRAIN-PERUSSAC; TISSUE-GANGLION.  
RX MEDLINE-89273551; PubMed-2597281;  
RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,  
RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.,  
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
RT "Purification of achatin-I from the atria of the African giant snail,  
RT Achatina fulica, and its possible function."  
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE-93014529; PubMed-1399265;  
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
RA Iwashita T., Nomoto K.,  
RT "Crystal structure and molecular conformation of achatin-I  
RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a  
RT D-amino acid residue."  
RL Int. J. Pept. Protein Res. 39:258-264(1992).  
CC -I- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY  
CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY  
CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE  
CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.  
DR PIR: A32480; A32480.  
KW Hormone; D-amino acid.  
FT MOD\_RES 2  
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 4;  
Best Local Similarity 50.0%; Pred. No. 8.9e+04;  
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GRGD 4  
11  
Db 1 GFD 4

RESULT 8  
PAP2\_PARMA STANDARD; PRT; 5 AA.  
ID PAP2\_PARMA  
AC P81864;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE PARDAXIN II (PXII) (FRAGMENT).

OS Pardachirus marmoratus (Red sea mores sole).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Soleoidae; Soleidae; Pardachirus.  
RN [1]  
RP SEQUENCE.  
RC TISSUE-SKIN SECRETION;  
RX MEDLINE-87057369; PubMed-3762138;  
RA Lazarevich P., Primor N., Isew L.M.,  
RT "Purification and pore-forming activity of two hydrophobic  
RT polypeptides from the secretion of the Red sea mores sole (Pardachirus  
RT marmoratus)."  
RL J. Biol. Chem. 261:16704-16713(1986).  
CC -I- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT  
CC PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS  
CC IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.  
CC -I- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A Tetramer.  
CC -I- SUBCELLULAR LOCATION: SECRETED.  
CC -I- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.  
KW Toxin.  
FT NON\_TER  
SQ SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 5;  
Best Local Similarity 66.7%; Pred. No. 8.9e+04;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 GDF 5  
11  
Db 1 GFF 3

RESULT 9  
TRN3\_ECOLI STANDARD; PRT; 5 AA.  
ID TRN3\_ECOLI  
AC P13973;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE TRAM PROTEIN (FRAGMENT).  
GN TRAM.  
OS Escherichia coli.  
OC Plasmid IncFII R100.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-88227859; PubMed-2836369;  
RA Inamoto S., Yoshioke Y., Ohtsubo E.,  
RT "Identification and characterization of the products from the trau  
RT and trau genes of plasmid R100."  
RL J. Bacteriol. 170:2749-2757(1988).  
CC -I- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION  
CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.  
CC -I- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -I- SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.  
CC -----  
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CC -----  
DR EMBL: M20941; NOT\_ANNOTATED\_CDS.  
DR PIR: A32014; A32014.  
KW Conjugation; Plasmid; DNA-binding.  
FT NON\_TER  
SQ SEQUENCE 5 AA; 634 MW; 6B1B1AA4435000000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 5;  
Best Local Similarity 33.3%; Pred. No. 8.9e+04;  
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RGD 4  
1  
DB 1 KND 3

RESULT 10

FLRF\_HIRME STANDARD; PRT; 4 AA.

AC P42561;  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFAMIDE.  
OS Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;  
OC Atychobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.

RP SEQUENCE.  
RC SPECIES-H.MEDICINALIS;  
RX MEDLINE-92195954; PubMed-1686933;  
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
RT "Identification of Rfamide neuropeptides in the medicinal leech."  
RL Peptides 12:897-908(1991).

RN [2]  
RP SEQUENCE.  
RC SPECIES-H.TRIVOLVIS; TISSUE-KIDNEY;  
RX MEDLINE-94286417; PubMed-7912428;  
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
RT "FMRfamide-related peptides from the kidney of the snail, Helisoma trivolvis."  
RL Peptides 15:31-36(1994).  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD.RES 4  
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match 21.2%; Score 7; DB 1; Length 4;  
Best Local Similarity 50.0%; Pred. No. 8.9e+04;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FV 6  
1  
DB 1 FL 2

RESULT 11

FMRF\_MACNI STANDARD; PRT; 4 AA.

AC P01162;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE FMRFAMIDE (PEAK C) (CARDIOEXCITATORY NEUROPEPTIDE).  
OS Macrocallista nimbosa (Sun-ray clam), Nerereis virens (Sandworm),  
OS Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heterococoncha; Veneroida;  
OC Veneroida; Veneridae; Macrocallista.

RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC SPECIES-M.NIMBOSA; TISSUE-CEREBRAL PEDAL, AND VISCERAL GANGLION;  
RX MEDLINE-77215956; PubMed-877582;  
RA Price D.A., Greenberg M.J.;  
RT "Structure of a molluscan cardioexcitatory neuropeptide."  
RL Science 197:670-671(1977).

RN [2]  
RP SEQUENCE, AND CHARACTERIZATION.

RC SPECIES-M.NIMBOSA; TISSUE-GANGLION;  
RX MEDLINE-78012038; PubMed-909875;  
RA Price D.A., Greenberg M.J.;  
RT "Purification and characterization of a cardioexcitatory neuropeptide from the central ganglia of a bivalve mollusc."  
RL Prep. Biochem. 7:261-281(1977).

RN [3]  
RP SEQUENCE.  
RC SPECIES-N.VIRENS; PubMed-2342992;  
RX MEDLINE-90259866;  
RA Krajauskas K.G., Price D.A.;  
RT "Authentic FMRfamide is present in the polychaete Nerereis virens."  
RL Peptides 11:75-77(1990).

RN [4]  
RP SEQUENCE.  
RC SPECIES-H.MEDICINALIS;  
RX MEDLINE-92195954; PubMed-1686933;  
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
RT "Identification of Rfamide neuropeptides in the medicinal leech."  
RL Peptides 12:897-908(1991).

RN [5]  
RP SEQUENCE.  
RC SPECIES-H.TRIVOLVIS; TISSUE-KIDNEY;  
RX MEDLINE-94286417; PubMed-7912428;  
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
RT "FMRfamide-related peptides from the kidney of the snail, Helisoma trivolvis."  
RL Peptides 15:31-36(1994).  
CC -1- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL ACTIVITIES INCLUDE AGGREGATION, INDUCTION, AND REGULARIZATION OF CARDIAC CONTRACTION.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.  
KW PIR; A01426; ECKN.  
DR PIR; A04048; A06048.  
KW Neuropeptide; Amidation.  
FT MOD.RES 4  
SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;

Query Match 21.2%; Score 7; DB 1; Length 4;  
Best Local Similarity 50.0%; Pred. No. 8.9e+04;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FV 6  
1  
DB 1 FM 2

RESULT 12

GRWL\_HUMAN STANDARD; PRT; 3 AA.

AC P01157;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last annotation update)  
DE GROWTH-MODULATING PEPTIDE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

RN [1]  
RP SEQUENCE.  
RX MEDLINE-77162369; PubMed-858356;  
RA Schlesinger D.H., Pickart L., Thaler M.M.;  
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine."  
RL Experientia 33:324-325(1977).  
CC -1- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.  
DR PIR; A01421; GRHL.  
SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 18.2%; Score 6; DB 1; Length 3;

Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1  
Db 1 G 1

RESULT 13

LDXE\_VIBRI ID LDXE\_VIBRI STANDARD: PRT: 3 AA.

AC P24272;

DT 01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE LONG-CHAIN-FATTY-ACID-LUCIFERIN-COMPONENT LIGASE (EC 6.2.1.19)

(ACYL-PROTEIN SYNTHETASE) (FRAGMENT).

GN LDXE.

OS Vibrio fischeri.

OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibri.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-91072226; Pubmed-2254256;

RA Swartman E., Kapoor S., Graham A.F., Melchen E.A.;

RT "A new Vibrio fischeri lux gene precedes a bidirectional termination

site for the lux operon."

RL J. Bacteriol. 172:6797-6802(1990).

CC -1- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.

CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE

FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS

SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.

CC -1- CATALYTIC ACTIVITY: ATP + AN ACID + PROTEIN -> AMP + PYROPHOSPHATE

CC + AN ACYL-PROTEIN THIOLESTER

CC -1- PATHWAY: SECOND STEP IN THE BIOLUMINESCENT FATTY ACID REDUCTASE

CC COMPLEX.

CC -----

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CC -----

DR EMBL: M62812; NOT\_ANNOTATED\_CDS.

KW Luminescence; Ligase.

FT NON\_TER 1

SO SEQUENCE 3 AA: 374 MW: 6AA3303000000000 CRC64;

Query Match 18.2%; Score 6; DB 1; Length 3;

Best Local Similarity 100.0%; Pred. No. 8.9e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 D 4

Db 3 D 3

RESULT 14

DCML\_PSECH ID DCML\_PSECH STANDARD: PRT: 4 AA.

AC P19916;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-DEC-1992 (Rel. 24, Last annotation update)

DE CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).

OS Pseudomonas carboxydohydrogena.

OC Bacteria; Proteobacteria.

RN [1]

RP SEQUENCE.

RX MEDLINE-90055678; Pubmed-2818128;

RA Kraut M., Hugendieck I., Herwig S., Meyer O.;

RT "Homology and distribution of CO dehydrogenase structural genes in

RT carboxydohydrogenic bacteria."

RL Arch. Microbiol. 152:335-341(1989).

CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR -> CO(2) + REDUCED

CC ACCEPTOR.

CC -1- CORFACTOR: MOLYBDENUM.

CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND

CC SMALL.

DR PIR: P10140; P10140.

KW Oxidoreductase; Molybdenum.

FT NON\_TER 4

SO SEQUENCE 4 AA: 441 MW: 7761876F00000000 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 8.9e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1

Db 2 G 2

RESULT 15

EOSI\_HUMAN ID EOSI\_HUMAN STANDARD: PRT: 4 AA.

AC P02731;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 21-JUL-1986 (Rel. 01, Last annotation update)

DE EOSINOPHILOTRACIC PEPTIDES.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RN [1]

RP SEQUENCE.

RX MEDLINE-76078412; Pubmed-1060093;

RA Goetzl E.J., Austen K.F.;

RT "Purification and synthesis of eosinophilic tetrapeptides of

human lung tissue: identification as eosinophil chemotactic factor of

anaphylaxis."

RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

CC -1- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG

CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS

CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING

CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE

CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.

DR PIR: A03190; E7H0L.

FT VARIANT 1

SO SEQUENCE 4 AA: 390 MW: 5B05862A00000000 CRC64;

Query Match 18.2%; Score 6; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 8.9e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1

Db 2 G 2

Search completed: March 6, 2001, 09:44:29  
Job time: 108 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 6, 2001, 09:42:22 ; Search time 19.02 Seconds  
(without alignments)  
36.974 Million cell updates/sec

Title: US-09-081-522-4  
Perfect score: 33  
Sequence: 1 GRGDFV 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues  
Total number of hits satisfying chosen parameters: 13

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORNITHINE:\*  
9: SP\_PLANT:\*  
10: SP\_PROTOZOA:\*  
11: SP\_VIRUS:\*  
12: SP\_VIRUS:\*  
13: SP\_VIRUS:\*  
14: SP\_UNCLASSIFIED:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	36.4	5	13	P82070
2	10	30.3	5	13	P82099
3	10	30.3	6	13	P82096
4	9	27.3	5	13	P82073
5	9	27.3	5	13	P82100
6	8	24.2	5	13	P82071
7	8	24.2	5	13	P82072
8	6	18.2	6	4	Q08720
9	5	15.2	6	10	P82181
10	5	15.2	6	10	P82182
11	5	15.2	6	10	P82541
12	4	12.1	6	11	Q08433
13	2	6.1	5	10	Q99007

## ALIGNMENTS

RESULT 1

P82070 PRELIMINARY; PRT; 5 AA.  
AC P82070:  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DE RUBELLIDIN 1.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE-SKIN SECRETION.  
RA Steinbörner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C., Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australian red tree frog 'Litoria rubella', the skin peptide profile as a probe for the study of evolutionary trends of amphibians.";  
RL Aust. J. Chem. 49:955-963(1996).  
CC -1- FUNCTION: CACRIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC ACTIVITY.  
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
CC -1- MASS SPECTROMETRY: MW=598; METHOD=FAE.  
KW Amphibian skin.  
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 36.4%; Score 12; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 DF 5  
P82099 PRELIMINARY; PRT; 5 AA.  
AC P82099:  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DE ELECTRIN 3.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE-SKIN SECRETION.  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian tree frog Litoria rubella. Comparison with the skin peptides from Litoria rubella.";  
RL Aust. J. Chem. 52:0-0(1999).  
KW Amphibian skin; Amidation.  
FT MOD\_RES 5  
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 30.3%; Score 10; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FV 6  
DB 1 FV 2

RESULT 3  
 ID P82096 PRELIMINARY; PRT; 6 AA.  
 AC P82096; (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE ELECTRIN 1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-SKIN SECRETION;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella."  
 RL Aust. J. Chem. 52:0-0(1999).  
 KW Amphibian skin; Amidation.  
 FT MOD\_RES 6  
 SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 30.3%; Score 10; DB 13; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 FV 6  
 Db 1 FV 2

RESULT 4  
 ID P82073 PRELIMINARY; PRT; 5 AA.  
 AC P82073; (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE RUBELIDIN 3.2.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-SKIN SECRETION;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella."  
 RL Aust. J. Chem. 52:0-0(1999).  
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
 CC ANTI-BIOTIC ACTIVITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 KW Amphibian skin.  
 SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 27.3%; Score 9; DB 13; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 3.7e+05; Mismatches 1; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 GDF 5  
 Db 2 GPF 4

RESULT 5

P82100 PRELIMINARY; PRT; 5 AA.  
 ID P82100; (TREMBlrel. 13, Created)  
 AC P82100; (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE ELECTRIN 4.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-SKIN SECRETION;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella."  
 RL Aust. J. Chem. 52:0-0(1999).  
 KW Amphibian skin; Amidation.  
 FT MOD\_RES 5  
 SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 27.3%; Score 9; DB 13; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 3.7e+05; Mismatches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 FV 6  
 Db 1 FV 2

RESULT 6  
 ID P82071 PRELIMINARY; PRT; 5 AA.  
 AC P82071; (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE RUBELIDIN 2.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE. AND MASS SPECTROMETRY.  
 RC TISSUE-SKIN SECRETION;  
 RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 RT Litoria rubella: the skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians."  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
 CC ANTI-BIOTIC ACTIVITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 CC -1- MASS SPECTROMETRY: MW=626; METHOD=FAB.  
 KW Amphibian skin.  
 SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 24.2%; Score 8; DB 13; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 3.7e+05; Mismatches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 DF 5  
 Db 2 EF 3

RESULT 7  
ID P82072 PRELIMINARY; PRT; 5 AA.  
AC P82072;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE RBELLIDIN 3.1.  
OC Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
OC Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE-SKIN SECTION;  
RA Steinhilber S.T., Mahlitz P.A., Kaugh R.J., Bowie J.H., Gao C.,  
RA Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australian red tree frog  
RT 'Litoria rubella', the skin peptide profile as a probe for the study  
RT of evolutionary trends of amphibians.";  
RL Aust. J. Chem. 49:955-963(1996).  
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
CC ANTIBIOTIC ACTIVITY.  
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
CC -1- MASS SPECTROMETRY: MW=655; METHOD=FAH.  
KM Amphibian skin; Amadation.  
FT MOD RES 5  
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 24.2%; Score 8; DB 13; Length 5;  
Best Local Similarity 50.0%; Pred. No. 3.7e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 DE 5  
DB 2 EF 3

RESULT 8  
ID 008720 PRELIMINARY; PRT; 6 AA.  
AC 008720;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE Y PROTEIN (FRAGMENT).  
GN CREB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93010691; PubMed=1396344;  
RA Waeber G., Habener J.F.;  
RT "Novel testis germ cell-specific transcript of the CREB gene contains  
RT an alternatively spliced exon with multiple in-frame stop codons.";  
RL EMBL; X68994; CAA48780.1; -  
FT NON\_TER 1 6  
SQ SEQUENCE 6 AA; 695 MW; 67272EB9C735D000 CRC64;

Query Match 18.2%; Score 6; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 F 5  
DB 3 F 3

RESULT 9  
ID P82181 PRELIMINARY; PRT; 6 AA.  
AC P82181;  
DT 01-JUN-2000 (TREMBLrel. 14, Created)  
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)  
DE CHLOROPLAST 50S RIBOSOMAL PROTEIN L10 BETA (FRAGMENT).  
OS Spinacia oleracea (Spinach).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;  
OC Caryophyllales; Chenopodiaceae; Spinacia.  
OX NCBI\_TaxID=3562;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=CV, ALMARO; TISSUE=LEAF;  
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;  
RT "Identification of all the proteins in the large subunit of an  
RT organelle (chloroplast) ribosome.";  
RL J. Biol. Chem. 275:10000-10006(2000).  
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.  
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND OTHER PLASTIDS.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.  
DR INTERPRO: IPR002363;  
DR PROSITE: PS01109; RIBOSOMAL\_L10; 1.  
KM Ribosomal protein; Chloroplast; rRNA-binding.  
FT NON\_TER 6  
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 15.2%; Score 5; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2  
DB 4 R 4

RESULT 10  
ID P82182 PRELIMINARY; PRT; 6 AA.  
AC P82182;  
DT 01-JUN-2000 (TREMBLrel. 14, Created)  
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)  
DE CHLOROPLAST 50S RIBOSOMAL PROTEIN L10 GAMMA (FRAGMENT).  
OS Spinacia oleracea (Spinach).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;  
OC Caryophyllales; Chenopodiaceae; Spinacia.  
OX NCBI\_TaxID=3562;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=CV, ALMARO; TISSUE=LEAF;  
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;  
RT "Identification of all the proteins in the large subunit of an  
RT organelle (chloroplast) ribosome.";  
RL J. Biol. Chem. 275:10000-10006(2000).  
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.  
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND OTHER PLASTIDS.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.  
DR INTERPRO: IPR002363;  
DR PROSITE: PS01109; RIBOSOMAL\_L10; 1.  
KM Ribosomal protein; Chloroplast; rRNA-binding.  
FT NON\_TER 6  
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 15.2%; Score 5; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2  
DB 4 R 4

## RESULT 11

P82541 PRELIMINARY; PRT; 6 AA.  
AC P82541;  
DT 01-OCT-2000 (TRENBLREL. 15, Created)  
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)  
DT 01-OCT-2000 (TRENBLREL. 15, Last annotation update)  
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S19 BETA (FRAGMENT).  
OS Spinacia oleracea (Spinach).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;  
OC Caryophyllales; Chenopodiaceae; Spinacia.  
OX NCBI\_TaxID=3562;  
RN [1]  
RP SEQUENCE.

RC STRAIN-CV. ALMARO;  
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;  
RT "Identification of all the proteins in the small subunit of an  
RT organelle (chloroplast) ribosome."  
RL J. Biol. Chem. 0:0-0(2000).  
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND OTHER PLASTIDS.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
CC -1- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA  
CC FORM IS THE MINOR BASIC FORM.  
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.  
DR INTERPRO: IPR002222;  
DR PROSITE: PS00323; RIBOSOMAL\_S19; PARTIAL.  
DR RIBOSOMAL protein; Chloroplast.  
FT NON\_TER 6  
SQ SEQUENCE 6 AA; 732 MW; 63333735A41C000 CRC64;

Query Match 15.2%; Score 5; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2  
DB 2 R 2

## RESULT 12

Q08433 PRELIMINARY; PRT; 4 AA.  
AC Q08433;  
DT 01-NOV-1996 (TRENBLREL. 01, Created)  
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
DT 01-JAN-1999 (TRENBLREL. 09, Last annotation update)  
DE UDP-GUCCUNONOSYLTRANSFERASE, MICROSOVAL (EC 2.4.1.17) (UDPGR)  
OS (FRAGMENT).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=GUNN;  
RX MEDLINE=91282758; PubMed=1840486;  
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;  
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the  
RT hyperbilirubinemic Gunn rat."  
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).  
CC -1- FUNCTION: UDPGR IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND

CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENDOGENOUS COMPOUNDS.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOOME.

DR EMBL, S38636; AAB19259.1;  
KW Transferase; Glycosyltransferase; Microsome; Multigene family.  
FT NON\_TER 1  
FT NON\_TER 4  
SQ SEQUENCE 4 AA; 473 MW; 633732CA20000000 CRC64;

Query Match 12.1%; Score 4; DB 11; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 V 6  
DB 2 V 2

## RESULT 13

Q99007 PRELIMINARY; PRT; 5 AA.  
AC Q99007;  
DT 01-NOV-1996 (TRENBLREL. 01, Created)  
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)  
DE ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).  
GN AMYL.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;  
RX MEDLINE=9129704; PubMed=1831055;  
RA Jacobsen J.V., Close T.J.;  
RT "Control of transient expression of chimeric genes by gibberellic  
RT acid and abscisic acid in protoplasts prepared from mature barley  
RT aleurone layers."  
RL Plant Mol. Biol. 16:713-721(1991).  
CC -1- CATALYTIC ACTIVITY: ENDOXYDOLYSIS OF 1,4-ALPHA-GLUCOSIDIC  
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.  
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.  
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN  
CC BARLEY.  
DR EMBL, X54643; CA38455.1;  
KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;  
KW Calcium; Multigene family.  
FT NON\_TER 5  
SQ SEQUENCE 5 AA; 600 MW; 61E3344D6F00000 CRC64;

Query Match 6.1%; Score 2; DB 10; Length 5;  
Best Local Similarity 0.0%; Pred. No. 3.7e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2  
DB 4 K 4

Search completed: March 6, 2001, 09:43:34  
Job time: 72 sec



XX Cheresch DA, Diefenbach B, Felding-Habermann B, Gurrath M;  
 PI Hoelzemann G, Jonczyk A, Kessler H, Melzer G, Mueller G;  
 DR WPI; 1994-009982/02.  
 XX  
 PT Compn. contg. cyclopenta- or hexa-peptide - inhibits adhesion of  
 animal cells, used in the treatment and prophylaxis of e.g.  
 thrombosis, tumours, osteoporosis or inflammation  
 PS  
 PS Claim 1; Page 7; 9pp; English.  
 XX  
 CC The sequences given in R45370-87 are cyclopenta- and  
 CC cyclohexapeptides which act to inhibit adhesion between animal cells.  
 CC A composition containing these peptides may be used in the  
 CC treatment and prophylaxis of thrombosis, myocardial infarction,  
 CC apoplexy, arteriosclerosis, inflammation, angina pectoris,  
 CC osteoporosis and/or tumour. They are used to induce an adhesion-  
 CC receptor antagonist effect in the subject, to inhibit cell adhesion,  
 CC and in the formation of osteoclasts. They may also be used in wound  
 CC healing compositions and to block beta-3 integrin fibrogen binding.  
 XX  
 SQ Sequence 5 AA:

Query Match 100.0%; Score 27; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2,1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDFV 5  
 |||||  
 Db 1 rgdfv 5

## RESULT 2

R45384  
 ID R45384 standard; Protein; 5 AA.

XX AC R45384;

XX DT 06-JUL-1994 (first entry);

XX DE Cell adhesion inhibition peptide (o).

XX KW Cyclopentapeptide; cyclohexapeptide; inhibition; adhesion;

KW animal; somatic; cell; thrombosis; myocardial infarction;

KW apoplexy; arteriosclerosis; inflammation; angina pectoris;

KW osteoporosis; tumour; adhesion-receptor antagonist; osteoclast;

KW wound healing; beta-3 integrin; fibrogen binding.

XX OS Synthetic.

XX FT Key

FT Modified-site 1 Location/Qualifiers  
 FT /note- "Amide linkage to Val5 forming a cyclic peptide"

FT MISC-difference 4 /note- "D-form residue"

FT Modified-site 5 /note- "Amide linkage to Arg1 forming a cyclic peptide"

XX EP578083-A.  
 PD 12-JAN-1994.

XX PF 26-JUN-1993; 93EP-0110232.

XX PR 06-JUL-1992; 92US-0909367.

XX PR 24-FEB-1993; 93US-0022024.

XX PA (MERE) MERCK PATENT GMBH.  
 XX Cheresch DA, Diefenbach B, Felding-Habermann B, Gurrath M;  
 PI Hoelzemann G, Jonczyk A, Kessler H, Melzer G, Mueller G;

XX WPI; 1994-009982/02.  
 XX  
 PT Compn. contg. cyclopenta- or hexa-peptide - inhibits adhesion of  
 animal cells, used in the treatment and prophylaxis of e.g.  
 thrombosis, tumours, osteoporosis or inflammation  
 PS  
 PS Claim 1; Page 7; 9pp; English.  
 XX  
 CC The sequences given in R45370-87 are cyclopenta- and  
 CC cyclohexapeptides which act to inhibit adhesion between animal cells.  
 CC A composition containing these peptides may be used in the  
 CC treatment and prophylaxis of thrombosis, myocardial infarction,  
 CC apoplexy, arteriosclerosis, inflammation, angina pectoris,  
 CC osteoporosis and/or tumour. They are used to induce an adhesion-  
 CC receptor antagonist effect in the subject, to inhibit cell adhesion,  
 CC and in the formation of osteoclasts. They may also be used in wound  
 CC healing compositions and to block beta-3 integrin fibrogen binding.  
 XX  
 SQ Sequence 5 AA:

Query Match 100.0%; Score 27; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2,1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDFV 5  
 |||||  
 Db 1 rgdfv 5

## RESULT 3

R45386  
 ID R45386 standard; Protein; 5 AA.

XX AC R45386;

XX DT 06-JUL-1994 (first entry)

XX DE Cell adhesion inhibition peptide (q).

XX KW Cyclopentapeptide; cyclohexapeptide; inhibition; adhesion;

KW animal; somatic; cell; thrombosis; myocardial infarction;

KW apoplexy; arteriosclerosis; inflammation; angina pectoris;

KW osteoporosis; tumour; adhesion-receptor antagonist; osteoclast;

KW wound healing; beta-3 integrin; fibrogen binding.

XX OS Synthetic.

XX FT Key

FT Modified-site 1 Location/Qualifiers  
 FT /note- "Amide linkage to Val5 forming a cyclic peptide"

FT Modified-site 5 /note- "D-form residue, Amide linkage to Arg1 forming  
 a cyclic peptide"

XX EP578083-A.  
 PD 12-JAN-1994.

XX PF 26-JUN-1993; 93EP-0110232.

XX PR 06-JUL-1992; 92US-0909367.

XX PR 24-FEB-1993; 93US-0022024.

XX PA (MERE) MERCK PATENT GMBH.

XX Cheresch DA, Diefenbach B, Felding-Habermann B, Gurrath M;  
 PI Hoelzemann G, Jonczyk A, Kessler H, Melzer G, Mueller G;  
 DR WPI; 1994-009982/02.

PT Compn. contg. cyclopenta- or hexa-peptide - inhibits adhesion of

PT animal cells, used in the treatment and prophylaxis of e.g.  
 PT thrombosis, tumours, osteoporosis or inflammation  
 XX  
 PS Claim 1; Page 7; 9pp; English.  
 CC  
 CC The sequences given in R45370-87 are cyclopenta- and  
 CC cyclohexapeptides which act to inhibit adhesion between animal cells.  
 CC A composition containing these peptides may be used in the  
 CC treatment and prophylaxis of thrombosis, myocardial infarction,  
 CC apoplexy, arteriosclerosis, inflammation, angina pectoris,  
 CC osteoporosis and/or tumour. They are used to induce an adhesion-  
 CC receptor antagonist effect in the subject, to inhibit cell adhesion,  
 CC and in the formation of osteoclasts. They may also be used in wound  
 CC healing compositions and to block beta-3 integrin fibrogen binding.  
 CC  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 27; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 RGDFFV 5  
 DB 1 rgdfv 5  
 RESULT 4  
 R45387  
 ID R45387 standard; Protein; 5 AA.  
 AC R45387;  
 XX  
 DT 06-JUL-1994 (first entry)  
 XX  
 DE Cell adhesion inhibitor peptide (r).  
 XX  
 KW Cyclopentapeptide; cyclohexapeptide; inhibition; adhesion;  
 KW animal; somatic; cell; thrombosis; myocardial infarction;  
 KW apoplexy; arteriosclerosis; inflammation; angina pectoris;  
 KW osteoporosis; tumour; adhesion-receptor antagonist; osteoclast;  
 KW wound healing; beta-3 integrin; fibrogen binding.  
 XX  
 OS Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT Modified-site 1  
 FT Msc-difference 3 /note- "Amide linkage to Val5 forming a cyclic peptide"  
 FT Modified-site 5 /note- "D-form residue"  
 FT Modified-site 5 /note- "Amide linkage to Arg1 forming a cyclic peptide"  
 XX  
 PN EP578083-A.  
 XX  
 PD 12-JAN-1994.  
 XX  
 PE 26-JUN-1993; 93EP-0110232.  
 XX  
 PR 06-JUL-1992; 92US-0909367.  
 PR 24-FEB-1993; 93US-0022024.  
 XX  
 PA (MERE ) MERCK PATENT GMBH.  
 XX  
 PI Cheresch DA, Diefenbach B, Felding-Habermann B, Gurrath M;  
 PI Hoelzemann G, Jonczyk A, Kessler H, Meizer G, Mueller G;  
 XX  
 WPI; 1994-009982/02.  
 XX  
 PT Compens. contg. cyclopenta- or hexa-peptide - inhibits adhesion of  
 PT animal cells, used in the treatment and prophylaxis of e.g.  
 PT thrombosis, tumours, osteoporosis or inflammation  
 XX

PS Claim 1; Page 7; 9pp; English.  
 XX  
 CC The sequences given in R45370-87 are cyclopenta- and  
 CC cyclohexapeptides which act to inhibit adhesion between animal cells.  
 CC A composition containing these peptides may be used in the  
 CC treatment and prophylaxis of thrombosis, myocardial infarction,  
 CC apoplexy, arteriosclerosis, inflammation, angina pectoris,  
 CC osteoporosis and/or tumour. They are used to induce an adhesion-  
 CC receptor antagonist effect in the subject, to inhibit cell adhesion,  
 CC and in the formation of osteoclasts. They may also be used in wound  
 CC healing compositions and to block beta-3 integrin fibrogen binding.  
 CC  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 27; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 RGDFFV 5  
 DB 1 rgdfv 5  
 RESULT 5  
 R82387  
 ID R82387 standard; peptide; 5 AA.  
 AC R82387;  
 XX  
 DT 03-MAY-1996 (first entry)  
 XX  
 DE Cyclic integrin alpha-v-beta-3 inhibitor peptide no. 62184.  
 XX  
 KW Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;  
 KW fibrinogen; inflammation; apoptosis; restenosis; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 PN WO955543-A1.  
 XX  
 PD 28-SEP-1995.  
 XX  
 PE 09-MAR-1995; 95WO-US03035.  
 XX  
 PR 30-DEC-1994; 34US-0366665.  
 PR 18-MAR-1994; 94US-0210715.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Brooks P, Cheresch DA;  
 XX  
 DR WPI; 1995-344463/44.  
 XX  
 PT Inhibition of angiogenesis in a tissue, e.g. following angioplasty  
 PT - by admin. of a compsn. comprising an alpha-v-beta3 antagonist,  
 PT useful for regression of established tumours, treating inflamed  
 PT tissue, etc.  
 XX  
 PS Claim 4; Page 47; 135pp; English.  
 XX  
 CC R82386-96 are a group of inhibitor peptides of integrin alpha-v-beta-3.  
 CC The inhibitor peptides may be administered in a compsn. and are useful  
 CC for inhibition of inflamed tissue angiogenesis, e.g. that associated  
 CC with rheumatoid arthritis, retinal angiogenesis associated with  
 CC diabetic retinopathy, that associated with haemangioma, solid  
 CC tumours, or solid tumour metastases. The alpha-v-beta-3 agonists  
 CC are also useful to induce apoptosis in neovascuature in a tissue.  
 CC The inhibitor peptides are pref. cyclic and contain an RGD sequence.  
 CC  
 SQ Sequence 5 AA;  
 XX

Query Match 100.0%; Score 27; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDV 5  
 |||||  
 Db 1 rgdtv 5

## RESULT 6

R82389 R82389 standard; peptide; 5 AA.

XX R82389;

XX 03-MAR-1996 (first entry)

DE Cyclic integrin alpha-v-beta-3 inhibitor peptide no. 62187.

XX Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;

KW fibrinogen; inflammation; apoptosis; restenosis; cyclic.

XX Synthetic.

OS Key Location/Qualifiers

FT Misc-difference 4 /note="D-Val"

XX W09525543-A1.

XX 28-SEP-1995.

XX 09-MAR-1995; 95MO-US03035.

XX 30-DEC-1994; 94US-0366665.

XX 18-MAR-1994; 94US-0210715.

XX (SCRI) SCRIPS RES INST.

XX Brooks P, Cheresh DA;

XX WPI; 1995-344463/44.

PT Inhibition of angiogenesis in a tissue, e.g. following angioplasty

PT - by admin. of a compsn. comprising an alpha-v-beta3 antagonist,

PT useful for regression of established tumours, treating inflamed

PT tissue, etc.

XX Claim 4; Page 47; 135pp; English.

XX R82386-96 are a group of inhibitor peptides of integrin alpha-v-beta-3.

CC The inhibitor peptides may be administered in a compsn. and are useful

CC for inhibition of inflamed tissue angiogenesis, e.g. that associated

CC with rheumatoid arthritis, retinal angiogenesis associated with

CC tumours, or solid tumour metastases. The alpha-v-beta-3 antagonists

CC are also useful to induce apoptosis in neovasculture in a tissue.

CC The inhibitor peptides are pref. cyclic and contain an RGD sequence.

XX Sequence 5 AA;

## Query Match

Best Local Similarity 100.0%; Score 27; DB 16; Length 5;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID W33057 standard; peptide; 5 AA.

XX W33057;

XX 26-JAN-1998 (first entry)

DE Alpha-v, beta-5 vitronectin receptor antagonist.

XX RGD containing peptide; antagonist; alpha-v, beta-5;

KW vitronectin receptor; inhibition; angiogenesis; inflammation;

KW rheumatoid arthritis; eye disease; diabetic retinopathy;

KW age related macular degeneration; ocular histoplasmosis;

KW retinopathy; prematurity; neovascular glaucoma;

KW corneal neovascular disorder; transplantation; herpetic; luetic;

KW keratitis; pterygium; neovascular pannus; haemangioma;

KW solid tumour; metastasis; cytokine; low toxicity;

KW vascular endothelial growth factor; epidermal growth factor; cyclic.

XX Synthetic.

OS Key Location/Qualifiers

FT Misc-difference 5 /note="D-form residue"

XX W09706791-A1.

XX 27-FEB-1997.

XX 13-AUG-1996; 96MO-US13194.

XX 14-AUG-1995; 95US-0514799.

XX 14-AUG-1996; 96ZA-0006886.

XX (SCRI) SCRIPS RES INST.

XX Brooks P, Cheresh DA, Friedlander M;

XX WPI; 1997-165019/15.

PT Inhibiting angiogenesis with an antagonist selective for the

PT alpha-v,beta-5 integrin receptor - e.g. antibody, RGD peptide or

PT organic mimetic, for treatment of inflammation, eye disease, tumours

PT etc.

XX Claim 5; Page 105; 126pp; English.

XX The present RGD containing peptide is an antagonist of the alpha-v,

CC beta-5 vitronectin receptor, which can be used to inhibit

CC angiogenesis in alpha-v, beta-5 containing tissue, specifically

CC angiogenesis as a result of inflammation (especially rheumatoid

CC arthritis), eye disease (especially diabetic retinopathy, age

CC related macular degeneration, ocular histoplasmosis, retinopathy of

CC prematurity or neovascular glaucoma), corneal neovascular disorders

CC (especially transplantation, herpetic or luetic keratitis,

CC pterygium and neovascular pannus associated with wearing contact

CC lenses), haemangioma, solid tumours and their metastases or

CC cytokines (especially vascular endothelial growth factor,

CC transforming growth factor alpha or epidermal growth factor). The

CC antagonist has the advantage of being very specific, affecting no

CC processes other than angiogenesis and therefore of relatively low

CC toxicity.

XX Sequence 5 AA;

SO Query Match 100.0%; Score 27; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDV 5  
 |||||  
 Db 1 rgdtv 5

RESULT 7  
 W33057



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RESULT      8
ID          W33055
AC          W33055;
DT          26-JAN-1998 (first entry)
XX
DE          Alpha-v, beta-5 vitronectin receptor antagonist.
XX
XX          RGD containing peptide; antagonist; alpha-v, beta-5;
KM          vitronectin receptor; inhibition; angiogenesis; inflammation;
KM          rheumatoid arthritis; eye disease; diabetic retinopathy;
KM          age related macular degeneration; ocular histioplasmosis;
KM          retinopathy; prematurity; neovascular glaucoma;
KM          corneal neovascular disorder; transplantation; herpetic; luetic;
KM          keratitis; pterygium; neovascular pannus; haemangioma;
KM          solid tumour; metastasis; cytokine; low toxicity;
KM          vascular endothelial growth factor;
KM          transforming growth factor alpha; epidermal growth factor; cyclic.
XX
XX          Synthetic.
OS
XX
FH          Key
FT          Misc-difference 4
FT          Location/Qualifiers
FT          /note- "D-form residue"
XX
XX          WO9706791-A1.
XX
XX          27-FEB-1997.
XX
XX          13-AUG-1996; 96WO-US13194.
XX
XX          14-AUG-1995; 95US-0514799.
XX          14-AUG-1996; 96ZA-0006886.
XX
XX          (SCRI ) SCRIpps RES INST.
XX
XX          Brooks P, Cheresh DA, Friedlander M;
PI          WPI; 1997-165019/15.
XX
XX          Inhibiting angiogenesis with an antagonist selective for the
PT          alpha-v,beta-5 integrin receptor - e.g. antibody, RGD peptide or
PT          organic mimetic, for treatment of inflammation, eye disease, tumours
PT          etc.
XX
XX          Claim 5; Page 105; 126pp; English.
XX
XX          The present RGD containing peptide is an antagonist of the alpha-v,
CC          beta-5 vitronectin receptor, which can be used to inhibit
CC          angiogenesis in alpha-v, beta-5 containing tissue, specifically
CC          angiogenesis as a result of inflammation (especially rheumatoid
CC          arthritis), eye disease (especially diabetic retinopathy, age
CC          related macular degeneration, ocular histioplasmosis, retinopathy of
CC          prematurity or neovascular glaucoma), corneal neovascular disorders
CC          (especially transplantation, herpetic or luetic keratitis,
CC          pterygium and neovascular pannus associated with wearing contact
CC          lenses), haemangioma, solid tumours and their metastases or
CC          cytokines (especially vascular endothelial growth factor,
CC          transforming growth factor alpha or epidermal growth factor). The
CC          antagonist has the advantage of being very specific, affecting no
CC          processes other than angiogenesis and therefore of relatively low
CC          toxicity.
XX
XX          Sequence 5 AA:
SQ

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Query Match      100.0%; Score 27; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.le+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY          1 RGDV 5
DB          1 RGDV 5
XX
RESULT      9
ID          W41099
AC          W41099;
DT          03-JUN-1998 (first entry)
XX
XX          Alpha-v beta-3 antagonist cyclic peptide 62184 (66203).
DE
XX          Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
KM          vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
KM          diabetic retinopathy; macular degeneration; restenosis; therapy;
KM          circular; cyclic.
XX
XX          Synthetic.
OS
XX
FH          Key
FT          Misc-difference 4
FT          Location/Qualifiers
FT          /note- "D-form residue"
XX
XX          WO9745137-A1.
XX
XX          04-DEC-1997.
XX
XX          30-MAY-1997; 97WO-US09158.
XX
XX          31-MAY-1996; 96US-0018733.
XX          31-MAY-1996; 96US-0018669.
XX
XX          (SCRI ) SCRIpps RES INST.
XX
XX          Brooks P, Cheresh DA;
PI          WPI; 1998-032334/03.
XX
XX          Packaging material containing polypeptide antagonist of alphav,
PT          beta3 integrin - used for inhibition of angiogenesis, and for
PT          treating tumours, inflammation, eye diseases etc.
XX
XX          Example 1; Page 46; 234pp; English.
XX
XX          This synthetic RGD-containing cyclic peptide, designated 62184 or
CC          66203, is a particularly preferred peptide that has integrin
CC          alpha-v beta-3 antagonist activity. It exhibits preferential
CC          inhibition of fibrinogen binding to the alpha-v beta-3 receptor.
CC          It can be prepared using standard solid-phase synthesis
CC          techniques. The invention relates to the discovery that
CC          angiogenesis is mediated by the specific vitronectin receptor
CC          alpha-v beta-3, and that inhibition of alpha-v beta-3 function
CC          inhibits angiogenesis. Claimed antagonists of alpha-v beta-3
CC          comprise C-terminal fragments (see W41083-94) of human or chicken
CC          matrix metalloproteinase-2, fusion polypeptides, cyclic or linear
CC          polypeptides, derivatised polypeptides, a monoclonal antibody or
CC          organic mimetic compound. They can be used to inhibit angiogenesis
CC          in inflamed tissue (for treatment of arthritis or rheumatoid
CC          arthritis), in solid tumours or metastases (particularly to induce
CC          regression or inhibit tumour growth), and in ocular disorders such
CC          as diabetic retinopathy and macular degeneration, as well as to
CC          treat restenosis (all claimed).
XX
XX          Sequence 5 AA:
SQ

```

```

Query Match      100.0%; Score 27; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.le+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 RGDFV 5  
| | | | |  
Db 1 rgdfv 5

## RESULT 10

W41101  
ID W41101 standard; Peptide: 5 AA.

AC W41101;

DT 08-JUN-1998 (first entry)

DE Alpha-v beta-3 antagonist cyclic peptide 62187.

XX Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;

KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;

KW diabetic retinopathy; macular degeneration; restenosis; therapy;

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 5 /note- "D-form residue"

XX W09745137-A1.

PD 04-DEC-1997.

PF 30-MAY-1997; 97WO-US09158.

PR 31-MAY-1996; 96US-0018733.

PR 31-MAY-1996; 96US-0015869.

PA (SCRI ) SCRIPPS RES INST.

PI Brooks P, Cheresch DA;

DR WPI: 1998-032334/03.

XX Packaging material containing polypeptide antagonist of alphav,

PT beta3 integrin - used for inhibition of angiogenesis, and for

PT treating tumours, inflammation, eye diseases etc.

XX Example 1; Page 48; 234pp; English.

PS This synthetic RGD-containing cyclic peptide, designated 62187,

XX is a particularly preferred peptide that has integrin

CC alpha-v beta-3 antagonist activity. It exhibits preferential

CC inhibition of fibrinogen binding to the alpha-v beta-3 receptor.

CC It can be prepared using standard solid-phase synthesis

CC techniques. The invention relates to the discovery that

CC angiogenesis is mediated by the specific vitronectin receptor

CC alpha-v beta-3, and that inhibition of alpha-v beta-3 function

CC inhibits angiogenesis. Claimed antagonists of alpha-v beta-3

CC comprise C-terminal fragments (see W41083-94) of human or chicken

CC matrix metalloproteinase-2, fusion polypeptides, cyclic or linear

CC polypeptides, derivatised polypeptides, a monoclonal antibody or

CC organic mimetic compound. They can be used to inhibit angiogenesis

CC in inflamed tissue (for treatment of arthritis or rheumatoid

CC arthritis), in solid tumours or metastases (particularly to induce

CC regression or inhibit tumour growth), and in ocular disorders such

CC as diabetic retinopathy and macular degeneration, as well as to

CC treat restenosis (all claimed).

CC Sequence 5 AA;

XX Query Match 100.0%; Score 27; DB 19; Length 5;

XX Best Local Similarity 100.0%; Pred. No. 2.1e+05;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDFV 5  
| | | | |  
Db 1 rgdfv 5

## RESULT 11

W41109  
ID W41109 standard; Peptide: 5 AA.

AC W41109;

DT 08-JUN-1998 (first entry)

DE Alpha-v beta-3 antagonist cyclic peptide 121974 (85189).

XX Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;

KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;

KW diabetic retinopathy; macular degeneration; restenosis; therapy;

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 5 /note- "valine residue NH2 terminal is

XX W09745137-A1.

PD 04-DEC-1997.

PF 30-MAY-1997; 97WO-US09158.

PR 31-MAY-1996; 96US-0018733.

PR 31-MAY-1996; 96US-0015869.

PA (SCRI ) SCRIPPS RES INST.

PI Brooks P, Cheresch DA;

DR WPI: 1998-032334/03.

XX Packaging material containing polypeptide antagonist of alphav,

PT beta3 integrin - used for inhibition of angiogenesis, and for

PT treating tumours, inflammation, eye diseases etc.

XX Example 1; Page 51; 234pp; English.

PS This synthetic RGD-containing cyclic peptide, designated 121974 or

XX 85189, is a particularly preferred peptide that has integrin

CC alpha-v beta-3 antagonist activity. It can be prepared using

CC standard solid-phase synthesis techniques. The invention relates

CC to the discovery that angiogenesis is mediated by the specific

CC vitronectin receptor alpha-v beta-3, and that inhibition of alpha-v

CC beta-3 function inhibits angiogenesis. Claimed antagonists of

CC alpha-v beta-3 comprise C-terminal fragments (see W41083-94) of

CC human or chicken matrix metalloproteinase-2, fusion polypeptides,

CC cyclic or linear polypeptides, derivatised polypeptides, a

CC monoclonal antibody or organic mimetic compound. They can be used

CC to inhibit angiogenesis in inflamed tissue (for treatment of

CC arthritis or rheumatoid arthritis), in solid tumours or metastases

CC (particularly to induce regression or inhibit tumour growth), and

CC in ocular disorders such as diabetic retinopathy and macular

CC degeneration, as well as to treat restenosis (all claimed).

CC Sequence 5 AA;

XX Query Match 100.0%; Score 27; DB 19; Length 5;

XX Best Local Similarity 100.0%; Pred. No. 2.1e+05;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDFV 5  
|||||  
Db 1 rgdfv 5

## RESULT 12

W41240  
ID W41240 standard; protein; 5 AA.

XX W41240;

AC 09-JUN-1998 (first entry)

XX Alpha-v-beta-5 antagonistic peptide 62184.

DE Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;

XX angiogenesis; tumour growth; restenosis; neovascularisation.

XX Synthetic.

OS Key Location/Qualifiers

FT MISC-difference 1..5 /note- "peptide is made cyclic via the first and

FT last residues"

FT MISC-difference 4 /note- "D-form residue"

XX W09745447-A1.

XX 04-DEC-1997.

XX 30-MAY-1997; 97MO-US03099.

XX 31-MAY-1996; 96US-0013733.

XX 31-MAY-1996; 96US-0013869.

XX (SCRI ) SCRIIPS RES INST.

XX Brooks P, Cheresh DA, Friedlander M;

XX WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav,  
PT betas integrin - used for inhibition of angiogenesis, and for  
PT treating tumours, inflammation, eye diseases etc.

XX Disclosure; Page 41; 117pp; English.

XX The present peptide represents an alpha-v-beta-5 integrin antagonists.

XX Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5

XX can inhibit angiogenesis. The specification describes a novel

XX labelled package that contains an inhibitor of angiogenesis i.e. an

XX alpha-v-beta-5 antagonising polypeptide that binds to integrin

XX alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.

XX The antagonists are used to inhibit angiogenesis in inflamed tissue, in

XX solid tumours or metastases, and in a wide range of ocular disorders

XX (e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or

XX corneal transplants). They are particularly used to induce regression or

XX to inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be

XX used to treat restenosis caused by migration of smooth muscle cells

XX following angioplasty and to reduce blood supply to selected tissues.

XX The antagonists particularly inhibit neovascularisation where this is

XX induced by cytokines, e.g. transforming growth factor alpha, epidermal

XX growth factor or especially vascular endothelial growth factor.

XX note: this sequence does not appear in the specification; it was created

XX using information provided.

XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDFV 5  
|||||  
Db 1 rgdfv 5

## RESULT 13

W41243  
ID W41243 standard; protein; 5 AA.

XX W41243;

AC 09-JUN-1998 (first entry)

XX Alpha-v-beta-5 antagonistic peptide 62187.

DE Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;

XX angiogenesis; tumour growth; restenosis; neovascularisation.

XX Synthetic.

OS Key Location/Qualifiers

FT MISC-difference 1..5 /note- "peptide is made cyclic via the first and

FT last residues"

FT MISC-difference 5 /note- "D-form residue"

XX W09745447-A1.

XX 04-DEC-1997.

XX 30-MAY-1997; 97MO-US09099.

XX 31-MAY-1996; 96US-0018733.

XX 31-MAY-1996; 96US-0015869.

XX (SCRI ) SCRIIPS RES INST.

XX Brooks P, Cheresh DA, Friedlander M;

XX WPI; 1998-041753/04.

XX Packaging material containing polypeptide antagonist of alphav,  
PT betas integrin - used for inhibition of angiogenesis, and for  
PT treating tumours, inflammation, eye diseases etc.

XX Disclosure; Page 41; 117pp; English.

XX The present peptide represents an alpha-v-beta-5 integrin antagonists.

XX Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5

XX can inhibit angiogenesis. The specification describes a novel

XX labelled package that contains an inhibitor of angiogenesis i.e. an

XX alpha-v-beta-5 antagonising polypeptide that binds to integrin

XX alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.

XX The antagonists are used to inhibit angiogenesis in inflamed tissue, in

XX solid tumours or metastases, and in a wide range of ocular disorders

XX (e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or

XX corneal transplants). They are particularly used to induce regression or

XX to inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be

XX used to treat restenosis caused by migration of smooth muscle cells

XX following angioplasty and to reduce blood supply to selected tissues.

XX The antagonists particularly inhibit neovascularisation where this is

XX induced by cytokines, e.g. transforming growth factor alpha, epidermal

XX growth factor or especially vascular endothelial growth factor.

XX note: this sequence does not appear in the specification; it was created

XX using information provided.

XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDFV 5  
11111  
Db 1 rgtdiv 5

RESULT 14  
W41247  
ID W41247 standard; protein; 5 AA.  
AC W41247;  
XX  
DT 09-JUN-1998 (first entry);  
XX  
DE Alpha-v-beta-5 antagonistic peptide.  
XX  
KW Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;  
KW angiogenesis; tumour growth; restenosis; neovascularisation.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT MISC-difference 4 /note= "D-form residue"  
XX  
PN W09745447-A1.  
XX  
PD 04-DEC-1997.  
XX  
PE 30-MAY-1997; 97WO-US09099.  
XX  
PR 31-MAY-1996; 96US-0016733.  
PR 31-MAY-1996; 96US-0015869.  
XX  
PA (SCRI ) SCRIPPS RES INST.  
XX  
PI Brooks P, Cheres DA, Friedlander M;  
XX  
DR WPI; 1998-041758/04.  
XX  
PT Packaging material containing polypeptide antagonist of alphav,  
PT betas integrin - used for inhibition of angiogenesis, and for  
PT treating tumours, inflammation, eye diseases etc.  
XX  
PS Disclosure; Page 38; 117pp; English.  
XX  
CC The present peptide represents an alpha-v-beta-5 integrin antagonists.  
CC Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5  
CC can inhibit angiogenesis. The specification describes a novel  
CC labelled package that contains an inhibitor of angiogenesis 1.e. an  
CC alpha-v-beta-5 antagonising polypeptide that binds to integrin  
CC alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.  
CC The antagonists are used to inhibit angiogenesis in inflamed tissue, in  
CC solid tumours or metastases, and in a wide range of ocular disorders  
CC (e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or  
CC corneal transplants). They are particularly used to induce regression or  
CC to inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be  
CC used to treat restenosis caused by migration of smooth muscle cells  
CC following angioplasty and to reduce blood supply to selected tissues.  
CC The antagonists particularly inhibit neovascularisation where this is  
CC induced by cytokines, e.g. transforming growth factor alpha, epidermal  
CC growth factor or especially vascular endothelial growth factor.  
CC note: this sequence does not appear in the specification; it was created  
CC using information provided.  
XX  
SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDFV 5  
11111  
Db 1 rgtdiv 5

RESULT 15  
W92307  
ID W92307 standard; peptide; 5 AA.  
AC W92307;  
XX  
DT 01-APR-1999 (first entry)  
XX  
DE Cyclic azapeptide #1.  
XX  
KW Cyclic peptide; azapeptide; integrin inhibitor; treatment; thrombosis;  
KW cardiac infarct; coronary heart disease; arteriosclerosis; tumour;  
KW osteoporosis; inflammation; infection; angiogenesis; antimicrobial;  
KW diagnosis; platelet metabolism; fibrinogen receptor; cancer; metastasis;  
KW intracellular signalling; Glib/Illa receptor; matrix metalloproteinase;  
KW vitronectin receptor.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1..5  
FT Modified-site /note= "The carboxy group of Val(5) is condensed onto  
FT the amino group of Arg(1) to form a cyclic  
FT peptide. Not true N- and C- terminus.  
FT Val(5) can be modified by N-Me"  
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FT Modified-site 2 /note= "aza-gly"  
XX  
FT MISC-difference 4 /note= "can be D-form residue"  
XX  
FT MISC-difference 5 /note= "can be D-form residue"  
XX  
PN DE19728524-A1.  
XX  
PD 07-JAN-1999.  
XX  
PE 04-JUL-1997; 97DE-1028524.  
XX  
PR 04-JUL-1997; 97DE-1028524.  
XX  
PA (MERE ) MERCK PATENT GMBH.  
XX  
PI Goodman SL, Jonezyk A, Kessler H, Schmitt J, Wermuth J;  
XX  
DR WPI; 1999-072017/07.  
XX  
PT New cyclic penta-peptide(s) containing aza-amino acid - are  
PT inhibitors of integrin-ligand interaction, used to treat e.g.  
PT thrombosis, cardiac infarct, coronary heart disease and tumours  
XX  
PS Claim 3a; Page 11; 12pp; German.  
XX  
CC This invention is concerned with novel cyclic peptides of formula  
CC cyclo(aarg-gly-aaasp-ax-ay) where aarg = Arg or aza-Arg, agly = Gly or  
CC aza-gly, aaasp = Asp or aza-asp, ax, ay = Ala, Asn, Asp, Cys, Gln,  
CC Glu, Gly, His, Ile, Leu, Lys, Met, Nle (norleucine), Orn (ornithine),  
CC Phe, Phg (phenylglycine), Pro, Ser, Thr, Tic (tetrahydroisquinoline-  
CC 3-carboxylic acid), Trp, Tyr, Val or NH-Q-CO, or the corresponding  
CC aza-amino acids, Q = 1-6C alkylene, at least one amino acid (aa) in the  
CC peptide has the alpha-carbon atom replaced by nitrogen also the aa may  
CC be derivatised and are coupled together by peptide bonds and optically  
CC active amino acids may be in D- or L-forms. The peptides are integrin  
CC inhibitors, specifically for treating and preventing thrombosis, cardiac  
CC infarct, coronary heart disease, arteriosclerosis, tumours, osteoporosis,  
CC inflammation and infections, or generally any disease where angiogenesis  
CC is involved, in human or veterinary medicine. The peptides also have  
CC antimicrobial activity, are used for diagnosis and location of thrombi,  
CC and for studying metabolism of platelets at different stages of

CC activation or intracellular signalling mechanisms of the fibrinogen  
CC receptor, and for affinity purification of integrins. The peptides  
CC inhibit interaction between the alpha v, beta 3 and beta 5 receptors with  
CC their ligands, e.g. they prevent binding of fibrinogen to the GPIIb/IIIa  
CC receptor, thus preventing metastatic spread of cancers, and prevent  
CC binding of matrix metalloproteinase to the vitronectin (alpha v beta 3)  
CC receptor. This sequence is a specific claimed example of a novel peptide  
CC of the invention.  
XX  
SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDFV 5  
|||  
Db 1 rgdfv 5

Search completed: March 6, 2001, 09:45:52  
Job time: 58 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 6, 2001, 09:44:53 ; Search time 19.1 Seconds  
(without alignments)  
4.701 Million cell updates/sec

Title: US-09-081-522-5

Perfect score: 27

Sequence: 1 RDEV 5

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 14061

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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5: /cgn2\_6/ptodata/2/1aa/BACKFILES1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	27	100.0	5	1	US-08-210-715-7
3	27	100.0	5	1	US-08-356-665-5
4	27	100.0	5	1	US-08-366-665-7
5	27	100.0	5	1	US-08-616-770-2
6	23	85.2	4	1	US-07-932-200-10
7	23	85.2	4	1	US-08-596-116A-68
8	23	85.2	4	2	US-08-668-871-12
9	23	85.2	4	2	US-08-669-683-12
10	23	85.2	4	2	US-08-387-749-10
11	23	85.2	4	2	US-08-335-832-25
12	23	85.2	4	2	US-08-753-781-20
13	23	85.2	4	2	US-08-361-864-28
14	23	85.2	4	4	PCT-US93-08231-10
15	23	85.2	4	5	5330911-12
16	23	85.2	5	1	US-08-315-0268-10
17	23	85.2	5	2	US-08-616-770-1
18	23	85.2	5	2	US-08-754-773B-10
19	23	85.2	5	3	US-09-141-127-23
20	23	85.2	5	3	US-09-155-721-1
21	23	85.2	5	3	US-09-155-721-2
22	23	85.2	5	3	US-09-155-721-4
23	23	85.2	5	3	US-09-155-721-5
24	23	85.2	5	3	US-09-155-721-6
25	23	85.2	5	3	US-09-155-721-7
26	23	85.2	5	3	US-09-155-721-8
27	23	85.2	5	3	US-09-155-721-9
28	23	85.2	5	5	5330911-13

29	22	81.5	5	3	US-08-694-387A-22	Sequence 22, Appl
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31	22	81.5	5	3	US-08-694-387A-24	Sequence 24, Appl
32	22	81.5	5	3	US-08-694-387A-25	Sequence 25, Appl
33	22	81.5	5	3	US-08-694-387A-27	Sequence 27, Appl
34	22	81.5	5	3	US-08-694-387A-29	Sequence 29, Appl
35	22	81.5	5	3	US-08-694-387A-30	Sequence 30, Appl
36	22	81.5	5	3	US-08-694-387A-32	Sequence 32, Appl
37	22	81.5	5	3	US-08-694-387A-33	Sequence 33, Appl
38	22	81.5	5	3	US-08-694-387A-34	Sequence 34, Appl
39	22	81.5	5	3	US-08-694-387A-35	Sequence 35, Appl
40	22	81.5	5	3	US-08-694-387A-37	Sequence 37, Appl
41	22	81.5	5	3	US-08-694-387A-38	Sequence 38, Appl
42	22	81.5	5	3	US-08-694-387A-39	Sequence 39, Appl
43	22	81.5	5	3	US-08-694-387A-40	Sequence 40, Appl
44	21	77.8	5	1	US-08-210-715-6	Sequence 6, Appl
45	21	77.3	5	1	US-08-210-715-9	Sequence 9, Appl

## ALIGNMENTS

RESULT 1  
US-08-210-715-5  
Sequence 5, Application US/08210715  
Patent No. 5753230  
GENERAL INFORMATION:  
APPLICANT: Brooks, Peter  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
INHIBITION OF ANGIOGENESIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESS: Research Institute  
STREET: 10665 NO. 5753230th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/210,715  
FILING DATE: 18-MAR-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 419.0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: circular  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..5  
OTHER INFORMATION: /label= cyclo  
OTHER INFORMATION: /note= "Cyclo signifies a cyclic peptide; lower  
case letters indicate a D-amino acid; capital  
letters indicate a L-amino acid."

US-08-210-715-5

Query Match 100.0%; Score 27; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. NO. 1.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDFV 5  
Db 1 RGDFV 5

RESULT 2  
US-08-210-715-7  
; Sequence 7, Application US/08210715  
; Patent No. 5753230  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; APPLICANT: Cheres, David A  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
; TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Office of Patent Counsel, The Scripps  
; ADDRESSEE: Research Institute  
; STREET: 10666 No. 5753230th Torrey Pines Road, TPC-8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/210.715  
; FILING DATE: 18-MAR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: TSRI 419.0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 554-2937  
; TELEFAX: (619) 554-6312  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: circular  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: Internal  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..5  
; OTHER INFORMATION: /label= cyclo  
; OTHER INFORMATION: /note= "Cyclo signifies a cyclic peptide; lower  
; OTHER INFORMATION: case letters indicate a D-amino acid; capital  
; OTHER INFORMATION: letters indicate a L-amino acid."  
US-08-210-715-7

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Best Local Similarity 100.0%; Pred. NO. 1.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDFV 5  
Db 1 RGDFV 5

RESULT 3  
US-08-366-665-5  
; Sequence 5, Application US/08366665  
; Patent No. 5766591  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; APPLICANT: Cheres, David A  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
; TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Office of Patent Counsel, The Scripps  
; ADDRESSEE: Research Institute  
; STREET: 10666 No. 5766591th Torrey Pines Road, TPC-8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/366,665  
; FILING DATE: 30-DEC-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/210,715  
; FILING DATE: 18-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: TSRI 419.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 554-2937  
; TELEFAX: (619) 554-6312  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: circular  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: Internal  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..5  
; OTHER INFORMATION: /label= cyclo  
; OTHER INFORMATION: /note= "Cyclo signifies a cyclic peptide; lower  
; OTHER INFORMATION: case letters indicate a D-amino acid; capital  
; OTHER INFORMATION: letters indicate a L-amino acid."  
US-08-366-665-5

Query Match 100.0%; Score 27; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. NO. 1.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDFV 5  
Db 1 RGDFV 5

RESULT 4  
US-08-366-665-7  
; Sequence 7, Application US/08366665  
; Patent No. 5766591  
; GENERAL INFORMATION:



APPLICANT: Brooks, Peter  
APPLICANT: Cheresn, David A  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 No. 576591ch Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/366,665  
FILING DATE: 30-DEC-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/210,715  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 419.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1-5  
OTHER INFORMATION: //label- cyclo  
OTHER INFORMATION: /note- "Cyclo signifies a cyclic peptide; lower  
OTHER INFORMATION: case letters indicate a D-amino acid; capital  
OTHER INFORMATION: letters indicate a L-amino acid."  
US-08-366-665-7

Query Match 100.0%; Score 27; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDFV 5  
DB 1 RGDFV 5

RESULT 5  
US-08-616-770-2  
Sequence 2, Application US/08616770  
Patent No. 5848692  
GENERAL INFORMATION:  
APPLICANT: Jonczyk, Alfred  
APPLICANT: Holzemann, Gunter  
APPLICANT: Felding-Habermann, Brunhilde  
APPLICANT: Rippmann, Friedrich  
APPLICANT: Diefenbach, Beate  
APPLICANT: Kessler, Horst  
APPLICANT: Haubner, Roland

APPLICANT: Wermuth, Jochen  
TITLE OF INVENTION: Cyclic Peptides Containing Arg-Gly-Asp, and  
TITLE OF INVENTION: Derivatives thereof, as Adhesion Inhibitors  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.  
STREET: 2200 Clarendon Boulevard, Suite 1400  
CITY: Arlington  
STATE: VA  
COUNTRY: U.S.A.  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/616,770  
FILING DATE: 15-MAR-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/220,858  
FILING DATE: 31-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 43 10 643.9  
FILING DATE: 01-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Heaney, Brian P.  
REGISTRATION NUMBER: 32,542  
REFERENCE/DOCKET NUMBER: MERCK 1566C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
TELEX: 64191  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: circular  
MOLECULE TYPE: peptide  
US-08-616-770-2

Query Match 100.0%; Score 27; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDFV 5  
DB 1 RGDFV 5

RESULT 6  
US-07-932-200-10  
Sequence 10, Application US/07932200  
Patent No. 536862  
GENERAL INFORMATION:  
APPLICANT: VENTON, DUANE L.  
APPLICANT: HOPFINGER, ANTON J.  
APPLICANT: LE BRETON, GUY  
TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING  
TITLE OF INVENTION: USEFUL PEPTIDES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEWMARK  
STREET: 419 SEVENTH STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/932,200  
FILING DATE: 21-AUG-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, IVER P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: VENTON-1B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3526  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-932-200-10

Query Match 85.2%; Score 23; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDF 4  
1111  
DB 1 RGDF 4

RESULT 7  
US-08-596-116A-68  
Sequence 68, Application US/08596116A  
Patent No. 5721213  
GENERAL INFORMATION:  
APPLICANT: SATO, Yoshimi  
APPLICANT: HAYASHI, Yoshio  
APPLICANT: KATADA, Jun  
TITLE OF INVENTION: No. 5721213el Peptides, Active as Inhibitors of  
TITLE OF INVENTION: Platelet Aggregation  
NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3+ Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: WordPerfect 6.1 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/596,116A  
FILING DATE: 30 JAN 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP94/01611  
FILING DATE: 29 SEP 1994  
APPLICATION NUMBER: JP 245541  
FILING DATE: 30 SEP 1993  
APPLICATION NUMBER: JP 50602  
FILING DATE: 22 MAR 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Toffenetti, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 2002/3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-429-1776

TELEFAX: 202-429-0796  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-596-116A-68

Query Match 85.2%; Score 23; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDF 4  
1111  
DB 1 RGDF 4

RESULT 8  
US-08-668-871-12  
Sequence 12, Application US/08668871  
Patent No. 5811389  
GENERAL INFORMATION:  
APPLICANT: Banwarth, Wilhelm  
APPLICANT: Gerber, Ferdinand  
APPLICANT: Grieder, Alfred  
APPLICANT: Knieringer, Andreas  
APPLICANT: Mueller, Klaus  
APPLICANT: Obrecht, Daniel  
TITLE OF INVENTION: TRI- AND TETRACYCLIC COMPOUNDS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07110-1199  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/668,871  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,508  
FILING DATE:  
APPLICATION NUMBER: CH 2725/92  
FILING DATE: 31-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Kass, Alan P.  
REGISTRATION NUMBER: 32142  
REFERENCE/DOCKET NUMBER: 3AN 4781/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-4205  
TELEFAX: (201) 235-5500  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-668-871-12

Query Match 85.2%; Score 23; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDF 4  
Db 1 RGDF 4

## RESULT 9

US-08-669-683-12  
Sequence 12, Application US/08669683  
Patent No. 581548  
GENERAL INFORMATION:  
APPLICANT: Bannwarth, Wilhelm  
APPLICANT: Gerber, Fernand  
APPLICANT: Grieder, Alfred  
APPLICANT: Krieger, Andreas  
APPLICANT: Mueller, Klaus  
APPLICANT: Obrecht, Daniel  
APPLICANT: Tizack, Arnold  
TITLE OF INVENTION: TRI- AND TETRACYCLIC COMPOUNDS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07110-1199  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,683  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,508  
FILING DATE:  
APPLICATION NUMBER: CH 2725/92  
FILING DATE: 31-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Kass, Alan P  
REGISTRATION NUMBER: 32142  
REFERENCE/DOCKET NUMBER: RAN 4781/1  
TELEPHONE: (201) 235-4205  
TELEFAX: (201) 235-3500  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-669-683-12

Query Match 85.2%; Score 23; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDF 4  
Db 1 RGDF 4

## RESULT 10

US-08-387-749-10  
Sequence 10, Application US/08387749  
Patent No. 5814460  
GENERAL INFORMATION:  
APPLICANT: VENTON, DUANE L.  
APPLICANT: HOPFINGER, ANTON J.

APPLICANT: LE BRETON, GUY  
TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 SEVENTH STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/387,749  
FILING DATE: 21-Feb-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08231  
FILING DATE: 09-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/932,200  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/813,315  
FILING DATE: 21-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/00891  
FILING DATE: 14-FEB-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/480,865  
FILING DATE: 14-FEB-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, IYER P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: VENTON-1C  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-387-749-10

Query Match 85.2%; Score 23; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDF 4  
Db 1 RGDF 4

## RESULT 11

US-08-335-832-25  
Sequence 25, Application US/08335832  
Patent No. 5925331  
GENERAL INFORMATION:  
APPLICANT: Dean, Richard T  
APPLICANT: Lister-James, John  
TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.  
STREET: 10 South Wacker Drive Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,832  
FILING DATE: 05-JAN-1995  
CLASSIFICATION: 42A  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5925331nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,216-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /label= ma  
OTHER INFORMATION: /note= "The amino terminus is modified by covalent  
US-08-335-832-25 linkage to an mercaptoacetyl group."  
Query Match 85.2%; Score 23; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RGDF 4  
Db 1 RGDF 4  
RESULT 12  
US-08-753-781-20  
Sequence 20, Application US/08753781C  
Patent No. 5951981  
GENERAL INFORMATION:  
APPLICANT: Markland Jr., Francis S.  
APPLICANT: Bush, Larry R.  
APPLICANT: Swenson, Stephen  
APPLICANT: Flores Sanchez, Eladio  
TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY  
FILE REFERENCE: DITI 124  
CURRENT APPLICATION NUMBER: US/08/753,781C  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 20  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: meercaptoacetyl  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:synthetic

US-08-753-781-20  
Query Match 85.2%; Score 23; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RGDF 4  
Db 1 RGDF 4  
RESULT 13  
US-08-361-864-28  
Sequence 28, Application US/08361864  
Patent No. 5977064  
GENERAL INFORMATION:  
APPLICANT: Dean, Richard T  
APPLICANT: Lister-James, John  
TITLE OF INVENTION: Multimeric Polyvalent Antithrombotic  
TITLE OF INVENTION: Agents  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Allegretti & Witcoff, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,864  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/955,466A  
FILING DATE: 19921002  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5977064nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,668  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-361-864-28  
Query Match 85.2%; Score 23; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RGDF 4  
Db 1 RGDF 4  
RESULT 14  
PCT-US93-08231-10  
Sequence 10, Application PC/TUS9308231  
GENERAL INFORMATION:  
APPLICANT: VENTON, DUANE L.  
APPLICANT: HOPFINGER, ANTON J.

Search completed: March 6, 2001, 09:45:18  
Job time: 25 sec

APPLICANT: LE BRETON, GUY  
TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING  
TITLE OF INVENTION: USEFUL PEPTIDES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 SEVENTH STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08231  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, IYER P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: VENTONIC.PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-08231-10

Query Match 85.2%; Score 23; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDF 4  
||||  
Db 1 RGDF 4

RESULT 15  
5330911-12  
Patent No. 5330911  
APPLICANT: HUBBELL, JEFFREY A.; MASSIA, STEPHEN P.; DESAI,  
NEIL P.  
TITLE OF INVENTION: SURFACES HAVING DESIRABLE CELL  
ADHESIVE EFFECTS  
NUMBER OF SEQUENCES: 27  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/527,198  
FILING DATE: 21-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 414,144  
FILING DATE: 28-SEP-1989  
SEQ ID NO: 12;  
LENGTH: 4  
5330911-12

Query Match 85.2%; Score 23; DB 5; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDF 4  
||||  
Db 1 RGDF 4

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:44:54 ; Search time 20.46 Seconds

(without alignments)  
16.594 Million cell updates/sec

Title: US-09-081-522-5

Perfect score: 27  
Sequence: 1 RGDFF 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 205

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	44.4	4	2 PT0711	T-cell receptor be
2	12	44.4	5	2 A32516	cholecystokinin-5
3	12	44.4	5	2 PQ0689	photosystem I 10.4
4	12	44.4	5	2 A44692	fulicin - giant Af
5	12	44.4	5	2 B61445	leu-enkephalin - b
6	12	44.4	5	2 A61445	Met-enkephalin - b
7	12	44.4	5	2 PT0513	T-cell receptor be
8	12	44.4	5	2 PT0538	T-cell receptor be
9	12	44.4	5	2 PT0703	T-cell receptor be
10	12	44.4	5	2 PT0690	T-cell receptor be
11	12	44.4	5	2 PT0573	T-cell receptor be
12	12	44.4	5	2 PT0679	T-cell receptor be
13	11	40.7	4	1 ECXAA	autho-RF amide neu
14	11	40.7	4	2 A25844	myosin-light-chain
15	11	40.7	4	2 S39390	ubiquitin - rat
16	11	40.7	4	2 S47552	cocoonase (EC 3.4.
17	11	40.7	5	2 B61168	T-cell receptor be
18	11	40.7	5	2 PT0525	T-cell receptor be
19	11	40.7	5	2 PT0608	T-cell receptor be
20	11	40.7	5	2 PT0695	T-cell receptor be
21	11	40.7	5	2 PT0700	T-cell receptor be
22	9	33.3	5	2 S68326	blood cell protein
23	9	33.3	5	4 A58728	seriawetlin W2 - S
24	8	29.6	4	2 D41654	hypothetical prote
25	8	29.6	4	2 PT0677	T-cell receptor be
26	8	29.6	5	2 A32014	tram protein - Esc
27	8	29.6	5	2 B45525	actin I - malaria
28	8	29.6	5	2 PT0540	T-cell receptor be
29	7	25.9	3	2 A23751	spinal cord peptid

30	7	25.9	4	2 ECNR	cardioexcitatory n
31	7	25.9	4	2 S09478	globulin IV alpha
32	7	25.9	4	2 A35779	neuropeptide Antho
33	7	25.9	4	2 A60418	FMRFamide - polych
34	7	25.9	4	2 B53284	T-cell receptor be
35	7	25.9	5	2 PT0508	Ig heavy chain CRD
36	7	25.9	5	2 PT0729	growth-modulating
37	6	22.2	3	2 GKRU	T-cell receptor be
38	6	22.2	3	2 A60898	growth-modulating
39	6	22.2	3	2 B23751	spinal cord peptid
40	6	22.2	3	2 PT0636	T-cell receptor be
41	6	22.2	3	2 PT0571	T-cell receptor be
42	6	22.2	3	2 S68328	blood cell protein
43	6	22.2	4	2 A32039	tyrosine-melanocyt
44	6	22.2	4	2 PL0140	carbon-monoxide de
45	6	22.2	4	2 A26209	protein-glutamine

#### ALIGNMENTS

##### RESULT 1

PT0711  
T-cell receptor beta chain V-D-J region (120-23) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0607; PT0674; PT0678; PT0570; PT0711; PT0710  
R:Peeney, A J  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
A:Reference number: PT0509; M01D:91277601  
A:Accession: PT0607  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-4 <FE3>  
A:Experimental source: newborn thymus, strain BALB/c, 120-23  
A:Accession: PT0674  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-4 <FE4>  
A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L  
A:Accession: PT0570  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-4 <FE4>  
A:Experimental source: day 19 fetal thymus, strain BALB/c, 141-1L  
A:Accession: PT0711  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-4 <FE5>  
A:Experimental source: newborn thymus, strain BALB/c (clones 161-2Ae and 161-2Ae)  
C:Keywords: T-cell receptor

Query Match 44.4% ; Score 12; DB 2; Length 4;  
Best Local Similarity 100.0% ; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GD 3  
DB 3 GD 4

RESULT 2  
A32516  
cholecystokinin-5 - dog  
N:Alternate names: CCK-5  
C:Species: Canis lupus familiaris (dog)

C>Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 18-Aug-2000  
C:Accession: A32516  
R:Shively, J.; Reese Jr, J.R.; Eusselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.  
Am. J. Physiol. 252, G272-G275, 1987  
A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intest  
A:Reference number: A32516; MUID:87153871  
A:Accession: A32516  
A:Molecule type: Protein  
A:Residues: 1-5 <SHI>  
C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecysto  
C:Superfamily: gastrin  
C:Keywords: amidated carboxyl end; neuropeptide  
F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 DF 4  
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Db 4 DF 5

RESULT 3  
P00689  
Photosystem I 10.4K H1 chain - common tobacco (fragment)  
C:Species: Nicotiana tabacum (common tobacco)  
C>Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
C:Accession: P00689  
R:Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.  
Plant Physiol. 102, 1259-1267, 1993  
A:Title: Molecular heterogeneity of photosystem I. psad, psae, psaf, psah and psal are a  
A:Reference number: P00687; MUID:94105345  
A:Accession: P00689  
A:Molecule type: protein  
A:Residues: 1-5 <OBO>  
C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GD 3  
||  
Db 3 GD 4

RESULT 4  
A44692  
fulicin - giant African snail  
C:Species: Achatina fulica (giant African snail)  
C>Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 11-Jul-1997  
C:Accession: A44692  
R:Ohta, N.; Kubota, I.; Takeo, T.; Shimomishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; No  
Biochem. Biophys. Res. Commun. 178, 486-493, 1991  
A:Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from t  
A:Reference number: A44692; MUID:91315471  
A:Accession: A44692  
A:Molecule type: protein  
A:Residues: 1-5 <OHT>  
C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide  
F:2/Modified site: D-asparagine (Asn) #status experimental  
F:5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 DFV 5  
||

Db 3 EFV 5  
RESULT 5  
B61445  
Leu-enkephalin - blue mussel  
C:Species: Mytilus edulis (blue mussel)  
C>Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000  
C:Accession: B61445  
R:Leung, M.K.; Stefano, G.B.  
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edu  
A:Reference number: A61445; MUID:84144823  
A:Accession: B61445  
A:Molecule type: protein  
A:Residues: 1-5 <LEU>  
A:Experimental source: pedal ganglia  
C:Keywords: neuropeptide; opioid peptide

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GDFV 5  
||  
Db 2 GDFL 5

RESULT 6  
A61445  
Met-enkephalin - blue mussel  
C:Species: Mytilus edulis (blue mussel)  
C>Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000  
C:Accession: A61445  
R:Leung, M.K.; Stefano, G.B.  
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edu  
A:Reference number: A61445; MUID:84144823  
A:Accession: A61445  
A:Molecule type: protein  
A:Residues: 1-5 <LEU>  
A:Experimental source: pedal ganglia  
C:Keywords: neuropeptide; opioid peptide

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GDFV 5  
||  
Db 2 GDFL 5

RESULT 7  
PT0513  
T-cell receptor beta chain V-D-J region (100-4AL) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0513; PT0606  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0513  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FEF>  
A:Experimental source: adult thymus, strain BALB/c, clone 100-4AL  
A:Accession: PT0606  
A:Status: translation not shown  
A:Molecule type: mRNA



A:Residues: 1-5 <FE2>  
A:Experimental source: newborn thymus, strain BALB/c, clone 120-1S  
C:Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GD 3  
Db 3 GD 4

## RESULT 8

PT0538  
T-cell receptor beta chain V-D-J region (126-1f) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0538; PT0539; PT0603  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0538  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: day 13 fetal thymus, strain BALB/c, clone 126-1f  
A:Accession: PT0603  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: newborn thymus, strain BALB/c, clone 126-1H  
C:Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GD 3  
Db 3 GD 4

## RESULT 9

PT0703  
T-cell receptor beta chain V-D-J region (135-1f) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0703  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0703  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GD 3  
Db 3 GD 4

## RESULT 10

PT0690  
T-cell receptor beta chain V-D-J region (140-1BD) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0690  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0690  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: day 18 fetal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GD 3  
Db 3 GD 4

## RESULT 11

PT0573  
T-cell receptor beta chain V-D-J region (141-1CC) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0573  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: day 19 fetal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GD 3  
Db 3 GD 4

## RESULT 12

PT0679  
T-cell receptor beta chain V-D-J region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0679; PT0708  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0679  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-5 <FE2>

A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-23  
A:Accession: P70708  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: newborn thymus, strain BALB/c, 161-2B  
C:Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GD 3  
||  
Db 3 GD 4

## RESULT 13

## ECXAA

antho-Ramide neuropeptide - sea anemone (Anthopleura elegantissima)  
C:Species: Anthopleura elegantissima  
C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 08-Dec-1995  
C:Accession: A26666  
R:Grimmelikhuizen, C.J.P.; Graff, D.  
Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986  
A:Title: Isolation of <Glu-Gly-Arg-Phe-NH2 (Antho-Ramide), a neuropeptide from sea anem  
A:Reference number: A26666; MUID:87092339  
A:Accession: A26666  
A:Molecule type: protein  
A:Residues: 1-4 <GR1>  
C:Comment: The function of this peptide is not known but it could act as a transmitter a  
C:Comment: Synthetic and natural peptides had identical properties.  
C:Superfamily: Ramide neuropeptide  
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 40.7%; Score 11; DB 1; Length 4;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGDF 4  
:| |  
Db 1 QGRF 4

## RESULT 14

## A25844

antho-RF amide neuropeptide - sea pansy (Renilla koellikeri)  
C:Species: Renilla koellikeri (Koelliker's sea pansy)  
C:Date: 21-May-1988 #sequence\_revision 30-Sep-1993 #text\_change 11-Jul-1997  
C:Accession: A25844  
R:Grimmelikhuizen, C.J.P.; Groeger, A.  
FEBS Lett. 211, 105-108, 1987  
A:Title: Isolation of the neuropeptide pGlu-Gly-Arg-Phe-amide from the pennatulid Renilla  
A:Reference number: A25844  
A:Accession: A25844  
A:Molecule type: protein  
A:Residues: 1-4 <GR1>  
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 40.7%; Score 11; DB 2; Length 4;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGDF 4  
:| |  
Db 1 QGRF 4

## RESULT 15

## S39390

myosin-light-chain kinase (EC 2.7.1.117), smooth muscle - turkey (fragment)  
C:Species: Meleagris gallopavo (common turkey)  
C:Date: 19-Mar-1997 #sequence\_revision 10-Oct-1997 #text\_change 07-May-1999  
C:Accession: S39390  
R:Komatsu, H.; Ikebe, M.  
Biochem. J. 286, 53-58, 1993  
A:Title: Affinity labelling of smooth-muscle myosin light-chain kinase with 5'-[p-(f-  
A:Reference number: S39390; MUID:94071841  
A:Accession: S39390  
A:Molecule type: protein  
A:Residues: 1-4 <KOM>  
A:Experimental source: gizzard  
C:Keywords: phosphotransferase; smooth muscle

Query Match 40.7%; Score 11; DB 2; Length 4;  
Best Local Similarity 66.7%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GDF 4  
||  
Db 2 GKF 4

Search completed: March 6, 2001, 09:47:29  
Job time: 155 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 6, 2001, 09:45:22 ; Search time: 12.72 Seconds

(Without alignments)  
12.694 Million cell updates/sec

Title: US-09-081-522-5

Perfect score: 27

Sequence: 1 RODEV 5

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.4	5	1	UXA4_CHLTR	P38005 chlamydia t
2	37.0	5	1	TPIS_CANFA	P34714 canis fami
3	33.3	5	1	PAP2_PARMA	P18654 pardachirus
4	29.6	5	1	TRM3_ECOLI	P13973 escherichia
5	25.9	4	1	FLRE_HIRME	P42561 hirudo medi
6	25.9	4	1	FMRF_MACNI	P01157 macrocallis
7	22.2	3	1	GRWK_HUMAN	P01157 homo sapien
8	22.2	3	1	LUXE_VIBRI	P24272 vibrio fisc
9	22.2	4	1	ACH1_ACHFU	P35904 achetina fu
10	22.2	4	1	DCML_PSECH	P19916 pseudomonas
11	22.2	4	1	FOST_HUMAN	P02731 homo sapien
12	22.2	4	1	FAK3_HIRME	P42562 hirudo medi
13	22.2	4	1	FAR4_HIRME	P42563 hirudo medi
14	22.2	5	1	AL14_CARMA	P41814 carclaus ma
15	22.2	5	1	BIOA_CITFR	P13071 citrobacter
16	22.2	5	1	BIOA_SALTY	P12677 salmonella
17	22.2	5	1	FAAP_ARPTE	P18853 artiposthi
18	22.2	5	1	SUGA_ACHDO	P19991 acheta dome
19	22.2	5	1	UC22_MAIZE	P08028 zea mays (m
20	22.2	5	1	UF01_MOUSE	P38639 mus musculu
21	18.5	4	1	TUFT_HUMAN	P18186 homo sapien
22	18.5	5	1	BIOB_SALTY	P12678 salmonella
23	18.5	5	1	PRCT_PPARAM	P01373 periplaneta
24	14.8	4	1	RM01_YEAST	P36515 saccharomyc
25	7.4	4	1	DCMS_PSECH	P19918 pseudomonas
26	7.4	5	1	BPP7_BOTIN	P30425 bothrops in
27	3.7	3	1	THYL_PIG	P01151 sus scrofa
28	3.7	5	1	BIOB_CITFR	P12997 citrobacter

## ALIGNMENTS

RESULT	ID	UXA4_CHLTR	STANDARD	PRT	5 AA
AC	P38005				
DT	01-OCT-1994	(Rel. 30, Created)			
DT	01-OCT-1994	(Rel. 30, last sequence update)			
DT	30-MAY-2000	(Rel. 39, last annotation update)			
DE	UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).				
OS	Chlamydia trachomatis.				
OC	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.				
RN	[1]				
RP	SEQUENCE.				
RC	STRAIN-L2/434/BJ;				
RA	Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,				
RA	Comanducci M., Christensen G., Birkelund S., Vitreou E., Ratti G.,				
RA	Pallini V.,				
RC	Submitted (SEP-1994) to the SWISS-PROT data bank.				
CC	-1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN				
CC	PROTEIN IS: 4.5, ITS MW IS: 28 KDA.				
FT	NON_TER	5			
SO	SEQUENCE	5 AA; 474 MW; 75BA865AA800000 CRC64;			

Query Match 44.4%; Score 12; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GD 3  
DB 3 GD 4

RESULT	ID	TPIS_CANFA	STANDARD	PRT	5 AA
AC	P34714				
DT	01-OCT-1996	(Rel. 34, Created)			
DT	01-OCT-1996	(Rel. 34, last sequence update)			
DT	15-JUL-1998	(Rel. 36, last annotation update)			
DE	TIROSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).				
OS	TP1.				
OC	Canis familiaris (Dog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE-HEART;				
RX	MEDLINE-98163340; Pubmed-9504812;				
RA	Dunn M.J., Corbett J.M., Wheeler C.H.;				
RT	"HSC-2DPAGE and the two-dimensional gel electrophoresis database of				
RT	dog heart proteins."				
RL	Electrophoresis 18:2795-2802(1997).				
CC	-1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE - DIHYDROXY-				
CC	ACETONE PHOSPHATE.				
CC	-1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.				
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO THE TIROSEPHOSPHATE ISOMERASE FAMILY.				
DR	HSC-2DPAGE; P54714; DOG.				
DR	INTERPRO: IPR000552; -.				
DR	PROSITE: PS00171; TIM; PARTIAL.				
KW	Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;				
KW	Pentose shunt.				
FT	NON_TER	1			
FT	NON_TER	5			
SO	SEQUENCE	5 AA; 550 MW; 54444862C9A00000 CRC64;			

Query Match 37.0%; Score 10; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FV 5  
11.

Db 1 EV 2

RESULT 3

PAP2\_PAPMA STANDARD; PRT; 5 AA.

AC P81864;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, last sequence update)  
 DT 01-OCT-2000 (Rel. 40, last annotation update)  
 DE PARDAXIN II (PxiI) (FRAGMENT).  
 OS Pardachirus marmoratus (Red sea moose sole).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 CC Acanthomorphi; Acanthopterygii; Percomorpha; Pleuronectiformes;  
 CC Soleoidae; Soleidae; Pardachirus.

RN [1]  
 RP SEQUENCE.  
 RC TISSUE-SKIN SECRETION;  
 RX MEDLINE-87057369; PubMed-3782138;  
 RA Lazarovici P., Primor N., Loew L.M.;  
 RT "Purification and pore-forming activity of two hydrophobic  
 RT polypeptides from the secretion of the Red sea moose sole (Pardachirus  
 RT marmoratus).";  
 RL J. Biol. Chem. 261:16704-16713(1986).  
 CC -1- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT  
 CC PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS  
 CC IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.  
 CC -1- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A Tetramer.  
 CC -1- SUBCELLULAR LOCATION: SECRETED.  
 CC -1- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.  
 KW Toxin.  
 FT NON TER  
 SO SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 33.3%; Score 9; DB 1; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 8.9e+04;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GDF 4  
 Db 1 GFF 3

RESULT 4

TRM3\_ECOLI STANDARD; PRT; 5 AA.

AC P1973;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, last sequence update)  
 DT 15-DEC-1998 (Rel. 37, last annotation update)  
 DE TRAM PROTEIN (FRAGMENT).  
 GN TRAM.  
 OS Escherichia coli.  
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 CC Escherichia.

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-88227859; PubMed-2836369;  
 RA Iinamoto S., Yoshioaka Y., Ohtsubo E.;  
 RT "Identification and characterization of the products from the tram  
 RT and tram genes of plasmid R100";  
 RL J. Bacteriol. 170:2749-2757(1988).  
 CC -1- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION  
 CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -1- SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.

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CC -----  
 CC EMBL; M20941; -; NOT\_ANNOTATED\_CDS.  
 CC DR PIR; A32014; A32014.  
 CC KW Conjugation; Plasmid; DNA-binding.  
 CC FT NON TER  
 CC SO SEQUENCE 5 AA; 634 MW; 6B1B1AA43500000 CRC64;

Query Match 29.6%; Score 8; DB 1; Length 5;  
 Best Local Similarity 33.3%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RGD 3  
 Db 1 KND 3

RESULT 5

FLRF\_HIRME STANDARD; PRT; 4 AA.

AC P42561;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, last sequence update)  
 DT 01-NOV-1995 (Rel. 32, last annotation update)  
 DE FLRFAMIDE.  
 OS Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).  
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;  
 CC Arynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES-H.MEDICINALIS;  
 RX MEDLINE-92195934; PubMed-1686933;  
 RA Evans B.D., Pohl J., Karlsonis M.A., Calabrese R.L.;  
 RT "Identification of Rfamide neuropeptides in the medicinal leech.";  
 RT Peptides 12:897-908(1991).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES-H.TRIVOLVIS; TISSUE-KIDNEY;  
 RX MEDLINE-94286417; PubMed-7912428;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma  
 RT trivolvis.";  
 RL Peptides 15:31-36(1994).  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC CC Neuropeptide; Amidation.  
 CC FT MOD.RES 4  
 CC SO SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match 25.9%; Score 7; DB 1; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 EV 5  
 Db 1 FL 2

RESULT 6

FMRF\_MACNI STANDARD; PRT; 4 AA.

AC P01162;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, last sequence update)  
 DT 15-JUL-1998 (Rel. 36, last annotation update)  
 DE FMRFAMIDE (PEAK C) (CARDIOEXCITATORY NEUROPEPTIDE).  
 OS Macrocallista nimbosa (Sun-ray clam), Neris virens (Sandworm),  
 OS Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconcha; Veneroida;  
 OC Veneroidae; Veneridae; Macrocallista.  
 [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC SPECIES-M.NIMBOSA; TISSUE-CEREBRAL PEDAL, AND VISCERAL GANGLION;  
 RX MEDLINE-77215956; PubMed-877582;  
 RA Price D.A., Greenberg M.J.;  
 RT "Structure of a molluscan cardioexcitatory neuropeptide."; *Science* 197;670-671(1977).  
 RL [2]  
 RP SEQUENCE, AND CHARACTERIZATION.  
 RC SPECIES-M.NIMBOSA; TISSUE-GANGLION;  
 RX MEDLINE-78012038; PubMed-909875;  
 RA Price D.A., Greenberg M.J.;  
 RT "Purification and characterization of a cardioexcitatory neuropeptide from the central ganglia of a bivalve mollusc."; *Prep. Biochem.* 7;261-281(1977).  
 RL [3]  
 RP SEQUENCE.  
 RC SPECIES-N.VIRENS;  
 RX MEDLINE-90259866; PubMed-2342992;  
 RA Kravtchak K.G., Price D.A.;  
 RT "Authentic FMRFamide is present in the polychaete *Nereis virens*."; *Peptides* 11;75-77(1990).  
 RL [4]  
 RP SEQUENCE.  
 RC SPECIES-H.MEDICINALIS;  
 RX MEDLINE-92195954; PubMed-1686933;  
 RA Evans B.D., Pohl J., Karlson M.A., Calabrese R.L.;  
 RT "Identification of RFamide neuropeptides in the medicinal leech."; *Peptides* 12;897-908(1991).  
 RL [5]  
 RP SEQUENCE.  
 RC SPECIES-H.TRIVOIVIS; TISSUE-KIDNEY;  
 RX MEDLINE-94286417; PubMed-7912428;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RT "FMRFamide-related peptides from the kidney of the snail, *Helisoma trivolvis*."; *Peptides* 15;31-36(1994).  
 RL [6]  
 CC -1- FUNCTION: MOXOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF CARDIAC CONTRACTION.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.  
 CC PIR: A01426; ECKR.  
 DR PIR: A60418; A60418.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 4 4  
 SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;  
 OY 4 FV 5  
 Db 1 FM 2  
 Query Match 25.9%; Score 7; DB 1; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RX MEDLINE-77162369; PubMed-858356;  
 RA Schlesinger D.H., Pickart L., Thaler M.M.;  
 RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine."; *Experientia* 33;324-325(1977).  
 RL [7]  
 CC -1- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.  
 DR PIR: A01421; GKRU.  
 SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;  
 OY 2 G 2  
 Db 1 G 1  
 Query Match 22.2%; Score 6; DB 1; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8  
 ID LUXE\_VIBRI STANDARD; PRT; 3 AA.  
 AC P24272;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE LONG-CHAIN-FATTY-ACID--LUCIFERIN-COMPONENT LIGASE (EC 6.2.1.19) (ACYL-PROTEIN SYNTHETASE) (FRAGMENT).  
 GN LUXE.  
 OS *Vibrio fischeri*.  
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; *Vibrio*.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91072226; PubMed-2254256;  
 RA Swartzman E., Kapoor S., Graham A.F., Weighen E.A.;  
 RT "A new *Vibrio fischeri* lux gene precedes a bidirectional termination site for the lux operon."; *J. Bacteriol.* 172;5797-6802(1990).  
 RL [2]  
 CC -1- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRACARBOIC ACID. IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE FOR CONVERTING TETRACARBOIC ACID TO THE ALDEHYDE WHICH SERVES AS SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.  
 CC -1- CATALYTIC ACTIVITY: ATP + AN ACID + PROTEIN = AMP + PYROPHOSPHATE + AN ACYL-PROTEIN THIOLESTER.  
 CC -1- PATHWAY: SECOND STEP IN THE BIOLUMINESCENT FATTY ACID REDUCTASE COMPLEX.  
 CC -----  
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 CC -----  
 DR EMBL: M62812; NOT\_ANNOTATED\_CDS.  
 KW Bioluminescence; Ligase.  
 FT NON\_TER 1  
 SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;  
 OY 3 D 3  
 Db 3 D 3  
 Query Match 22.2%; Score 6; DB 1; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9  
 ID ACHI\_ACHFU STANDARD; PRT; 4 AA.  
 AC ACHI\_ACHFU  
 ID ACHI\_ACHFU

AC P35904;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE ACHATIN-I.  
 OS Achatina fulica (Giant African snail).  
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylomatophora;  
 CC Achatinacea; Achatinidae; Achatina.  
 [1]  
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.  
 RC STRAIN-FERUSSAC; TISSUE-GANGLION;  
 RA MEDLINE=8927351; PubMed=2597281;  
 RA Kametani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,  
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-I. P.,  
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;  
 RT "Achatin-I, an endogenous neuropeptide tetrapeptide from Achatina  
 fulica Ferussac containing a D-amino acid residue."  
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).  
 [2]  
 RN CHARACTERIZATION.  
 RC STRAIN-FERUSSAC; TISSUE=HEART ATRIUM;  
 RA MEDLINE=91264856; PubMed=1675568;  
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
 RA Yoshida M., Harada A., Nuneoka Y., Kobayashi M.;  
 RT "Purification of achatin-I from the atria of the African giant snail,  
 Achatina fulica, and its possible function."  
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).  
 [3]  
 RN X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=93014529; PubMed=1399265;  
 RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
 RA Iwashita T., Nomoto K.;  
 RT "Crystal structure and molecular conformation of achatin-I  
 (H-Gly-D-phe-Ala-Asp-OH), an endogenous neuropeptide containing a  
 D-amino acid residue."  
 RL Int. J. Pept. Protein Res. 39:258-264(1992).  
 CC -I- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY  
 AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY  
 NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE  
 HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.  
 DR PIR: A32480; A32480.  
 KW Hormone; D-amino acid.  
 FT MOD.RES  
 FT SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;  
 SQ  
 Query Match 22.2%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2 G 2  
 Db 1 G 1  
 RESULT 10  
 ID DCML\_PSECH STANDARD; PRT; 4 AA.  
 AC P19916;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DE CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).  
 OS Pseudomonas carboxydohydrogena.  
 CC Bacteria; Proteobacteria.  
 [1]  
 RN SEQUENCE.  
 RP MEDLINE=90055678; PubMed=2818128;  
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;  
 RT "Homology and distribution of CO dehydrogenase structural genes in  
 carboxydophilic bacteria."  
 RL Arch. Microbiol. 152:335-341(1989).  
 CC -I- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR - CO(2) + REDUCED

CC ACCEPTOR.  
 CC -I- COFACTOR: MOLYBDENUM.  
 CC -I- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND  
 CC SMALL.  
 DR PIR: P10140; P10140.  
 KW Oxidoreductase; Molybdenum.  
 FT NON\_TER  
 FT SEQUENCE 4 AA; 441 MW; 7761E876F00000000 CRC64;  
 SQ  
 Query Match 22.2%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2 G 2  
 Db 2 G 2  
 RESULT 11  
 ID E0SI\_HUMAN STANDARD; PRT; 4 AA.  
 AC P02731;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last annotation update)  
 DE EOSINOPHILOTOXIC PEPTIDES.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 [1]  
 RN SEQUENCE.  
 RX MEDLINE=76078412; PubMed=1060093;  
 RA Goetzl E.J., Austen K.F.;  
 RT "Purification and synthesis of eosinophilotoxic tetrapeptides of  
 human lung tissue: identification as eosinophil chemotactic factor of  
 anaphylaxis."  
 RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).  
 CC -I- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG  
 (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS  
 (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING  
 EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE  
 OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.  
 DR PIR: A03190; EIBUL.  
 FT VARIANT 1  
 FT SEQUENCE 4 AA; 390 MW; 6B05862A00000000 CRC64;  
 SQ  
 Query Match 22.2%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2 G 2  
 Db 2 G 2  
 RESULT 12  
 ID FAR3\_HIRME STANDARD; PRT; 4 AA.  
 AC P42562;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FARFAMIDE-LIKE NEUROPEPTIDE YIRF-AMIDE.  
 OS Hirudo medicinalis (Medicinal leech).  
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;  
 CC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.  
 [1]  
 RN SEQUENCE.  
 RP MEDLINE=92195954; PubMed=1686933;  
 RA Evans B.D., Pohl J., Karlsonis M.A., Calabrese R.L.;

RT "Identification of Rfamlike neuropeptides in the medicinal leech."  
 RL Peptides 12:897-908(1991).  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC NEUROPEPTIDE: Amidation.  
 FT MOD\_RES 4  
 SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 22.2%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 F 4  
 Db 4 F 4

RESULT 13  
 FARP\_HIRME STANDARD; PRT; 4 AA.  
 ID FARP\_HIRME  
 AC P42563;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFAMIDE-LIKE NEUROPEPTIDE YMRF-AMIDE.  
 OS Hirudo medicinalis (Medicinal leech).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinoidea; Hirudiniformes; Hirudinales; Hirudo.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE-92195954; PubMed-1586933;  
 RA Evans B.D., Pohl J., Karlsson M.A., Calabrese R.L.;  
 RT "Identification of Rfamlike neuropeptides in the medicinal leech."  
 RL Peptides 12:897-908(1991).  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC NEUROPEPTIDE: Amidation.  
 FT MOD\_RES 4  
 SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 22.2%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 F 4  
 Db 4 F 4

RESULT 14  
 AL14\_CARMA STANDARD; PRT; 5 AA.  
 ID AL14\_CARMA  
 AC P81817;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CARCINOSTATIN 14.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;  
 RX MEDLINE-98121193; PubMed-9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas."  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.

CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC NEUROPEPTIDE: Amidation; Multigene family.  
 FT MOD\_RES 5  
 SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 22.2%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 F 4  
 Db 3 F 3

RESULT 15  
 BIOA\_CITFR STANDARD; PRT; 5 AA.  
 ID BIOA\_CITFR  
 AC P13071;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DE ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE  
 DE (EC 2.6.1.62) (7,8-DIAMINO-PELAGONIC ACID AMINOTRANSFERASE) (DAPA  
 DE AMINOTRANSFERASE) (FRAGMENT).  
 GN BIOA.  
 OS Citrobacter freundii.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Citrobacter.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-89005280; PubMed-2971595;  
 RA Shih D., Campbell A.;  
 RT "transcriptional regulation and gene arrangement of Escherichia coli,  
 RT Citrobacter freundii and Salmonella typhimurium biotin operons."  
 RL Gene 67:203-211(1988).  
 CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-  
 CC OXONONANOATE -> S-ADENOSYL-4-METHYLTHIO-2-OXOBUTANOATE +  
 CC 7,8-DIAMINONONANOATE.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- PATHWAY: BIOTIN BIOSYNTHESIS.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M21922; CAB25179.1; -  
 DR INTERPRO: IPR003954; -  
 DR PROSITE: PS00600; AA TRANSFER\_CLASS\_3; PARTIAL.  
 KW Biotin biosynthesis; transferase; aminotransferase;  
 KW Pyridoxal phosphate.  
 FT NON\_TER 5  
 SQ SEQUENCE 5 AA; 582 MW; 5AAB1BA6F00000 CRC64;

Query Match 22.2%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 D 3  
 Db 4 D 4

Search completed: March 6, 2001, 09:48:22

Tue Mar 6 09:57:32 2001

us-09-081-522-5.closed.rsp

Job time: 180 sec



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OM protein - protein search, using sw model

Run on: March 6, 2001, 09:44:54 ; Search time 32.72 seconds  
(without alignments)  
17.911 Million cell updates/sec

Title: US-09-081-522-5

Perfect score: 27

Sequence: 1 RGDV 5

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing:

Maximum Match 0%

Listing first 45 summaries

Database :  
1: SPRENBL\_15:\*  
2: sp.archaea:\*  
3: sp.bacteria:\*  
4: sp.fungi:\*  
5: sp.human:\*  
6: sp.invertebrate:\*  
7: sp.mammal:\*  
8: sp.mhc:\*  
9: sp.organelle:\*  
10: sp.phage:\*  
11: sp.plant:\*  
12: sp\_rodent:\*  
13: sp\_virus:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	44.4	5	13	P82070 litorea rub
2	10	37.0	5	13	P82099 litorea rub
3	9	33.3	5	13	P82073 litorea rub
4	9	33.3	5	13	P82100 litorea rub
5	8	29.6	5	13	P82071 litorea rub
6	8	29.6	5	13	P82072 litorea rub
7	4	14.8	5	11	Q08433 rattus norv
8	2	7.4	5	10	Q99007 hordeum vul

#### ALIGNMENTS

RESULT 1  
ID P82070 PRELIMINARY: PRT: 5 AA.  
AC P82070; 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)  
DE RUBELLIDIN 1.1.  
OS litorea rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
OC litorea.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE-SKIN SECRETION.  
RA Steinboerner S.T., Wadnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
RA Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australian red tree frog  
litorea rubella", the skin peptide profile as a probe for the study  
of evolutionary trends of amphibians.";  
RL Aust. J. Chem. 49:955-963(1996).  
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
ANTIBIOTIC ACTIVITY.  
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
CC -1- MASS SPECTROMETRY: MW=598; METHOD=FAE.  
KW Amphibian skin.  
SQ SEQUENCE 5 AA: 598 MW: 6DD9C9CAB2A00000 CRC64;

Query Match 44.4%; Score 12; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DF 4  
DB 2 DF 3

RESULT 2  
ID P82099 PRELIMINARY: PRT: 5 AA.  
AC P82099;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)  
DE ELECTRIN 3.  
OS litorea rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
OC litorea.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP TISSUE-SKIN SECRETION.  
RC TISSUE-SKIN SECRETION.  
RA Wadnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
litorea rubella. Comparison with the skin peptides from litorea  
rubella.";  
RL Aust. J. Chem. 52:0-0(1999).  
KW Amphibian skin; Amidation.  
FT MOD. RES 5  
SQ SEQUENCE 5 AA: 630 MW: 668761F2C9A00000 CRC64;

Query Match 37.0%; Score 10; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
DB 1 EV 2

RESULT 3  
ID P82073 PRELIMINARY: PRT: 5 AA.  
AC P82073;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE RUBELLIDIN 3.2.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-SKIN SECRETION.  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT 'Litoria rubella', the skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 52:0-0(1999).  
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
 CC -1- ANTIBIOTIC ACTIVITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 KW Amphibian skin.  
 SQ SEQUENCE 5 AA: 570 MW: 71A9C9C862A00000 CRC64;

Query Match 33.3%; Score 9; DB 13; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 3.7e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GDF 4  
 DB 2 GFF 4

RESULT 4  
 ID P82100 PRELIMINARY; PRT; 5 AA.  
 AC P82100;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE ELECRRIN 4.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-SKIN SECRETION.  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT 'Litoria rubella', the skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 52:0-0(1999).  
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
 CC -1- ANTIBIOTIC ACTIVITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 KW Amphibian skin; Amidation.  
 FT MOD\_RES 5  
 SQ SEQUENCE 5 AA: 616 MW: 61F2D1A059A00000 CRC64;

Query Match 33.3%; Score 9; DB 13; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 3.7e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 FV 5  
 DB 1 FI 2

RESULT 5  
 ID P82071 PRELIMINARY; PRT; 5 AA.  
 AC P82071;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE RUBELLIDIN 2.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE-SKIN SECRETION;  
 RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RT Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 RT 'Litoria rubella', the skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 49:555-963(1996).  
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
 CC -1- ANTIBIOTIC ACTIVITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 CC -1- MASS SPECTROMETRY: MW=626; METHOD=FAV.  
 KW Amphibian skin.  
 SQ SEQUENCE 5 AA: 626 MW: 6DD9C9CB10300000 CRC64;

Query Match 29.6%; Score 8; DB 13; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 3.7e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 DF 4  
 DB 2 EF 3

RESULT 6  
 ID P82072 PRELIMINARY; PRT; 5 AA.  
 AC P82072;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE RUBELLIDIN 3.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE-SKIN SECRETION;  
 RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RT Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 RT 'Litoria rubella', the skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 49:555-963(1996).  
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
 CC -1- ANTIBIOTIC ACTIVITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 CC -1- MASS SPECTROMETRY: MW=655; METHOD=FAV.  
 KW Amphibian skin; Amidation.  
 FT MOD\_RES 5  
 SQ SEQUENCE 5 AA: 656 MW: 71A9C9CB10300000 CRC64;

Query Match 29.6%; Score 8; DB 13; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 3.7e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 DF 4  
 DB 2 EF 3

```

RESULT 7
008433 PRELIMINARY; PRT; 4 AA.
AC 008433;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE, MICROSOFT (EC 2.4.1.17) (UDPGR)
DE (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUNN;
RA MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT hyperbilirubinemic Gunn rat."
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC -! FUNCTION: UDPGR IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -! CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -! SUBCELLULAR LOCATION: MICROSOFT.
DR EMBL; S38636; ABAB19259.1;
RW Transferase; Glycosyltransferase; Microsome; Multigene family.
FT NON_TER 1 1
FT NON_TER 4 4
SO SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

```

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Query Match 14.88; Score 4; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 5 V 5
DB 2 V 2

```

```

RESULT 8
099007 PRELIMINARY; PRT; 5 AA.
AC 099007;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).
GN AMY1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX MEDLINE=91329704; PubMed=1831055;
RX Jacobsen J.V., Close T.J.;
RT "Control of transient expression of chimeric genes by gibberellic
RT acid and abscisic acid in protoplasts prepared from mature barley
RT aleurone layers."
RL Plant Mol. Biol. 16:713-721(1991).
CC -! CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -! COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -! MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC BARLEY.
DR EMBL; X54643; CAAB38455.1;
RW Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family.

```

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FT NON_TER 5 5
SO SEQUENCE 5 AA; 500 MW; 61E3344DD6F00000 CRC64;

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Best Local Similarity 0.0%; Pred. No. 3.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 R 1
DB 4 K 4

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Search completed: March 6, 2001, 09:48:05
Job time: 191 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:45:52 ; Search time 30.08 Seconds  
(without alignments)  
5.684 Million cell updates/sec

Title: US-09-081-522-7

Perfect score: 27  
Sequence: 1 RGDV 5

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 14863

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

A.Geneseq\_36:\*

- 1: /SIDSI/gcgcdata/geneseq/geneseq/AA1980.DAT:\*
- 2: /SIDSI/gcgcdata/geneseq/geneseq/AA1981.DAT:\*
- 3: /SIDSI/gcgcdata/geneseq/geneseq/AA1982.DAT:\*
- 4: /SIDSI/gcgcdata/geneseq/geneseq/AA1983.DAT:\*
- 5: /SIDSI/gcgcdata/geneseq/geneseq/AA1984.DAT:\*
- 6: /SIDSI/gcgcdata/geneseq/geneseq/AA1985.DAT:\*
- 7: /SIDSI/gcgcdata/geneseq/geneseq/AA1986.DAT:\*
- 8: /SIDSI/gcgcdata/geneseq/geneseq/AA1987.DAT:\*
- 9: /SIDSI/gcgcdata/geneseq/geneseq/AA1988.DAT:\*
- 10: /SIDSI/gcgcdata/geneseq/geneseq/AA1989.DAT:\*
- 11: /SIDSI/gcgcdata/geneseq/geneseq/AA1990.DAT:\*
- 12: /SIDSI/gcgcdata/geneseq/geneseq/AA1991.DAT:\*
- 13: /SIDSI/gcgcdata/geneseq/geneseq/AA1992.DAT:\*
- 14: /SIDSI/gcgcdata/geneseq/geneseq/AA1993.DAT:\*
- 15: /SIDSI/gcgcdata/geneseq/geneseq/AA1994.DAT:\*
- 16: /SIDSI/gcgcdata/geneseq/geneseq/AA1995.DAT:\*
- 17: /SIDSI/gcgcdata/geneseq/geneseq/AA1996.DAT:\*
- 18: /SIDSI/gcgcdata/geneseq/geneseq/AA1997.DAT:\*
- 19: /SIDSI/gcgcdata/geneseq/geneseq/AA1998.DAT:\*
- 20: /SIDSI/gcgcdata/geneseq/geneseq/AA1999.DAT:\*
- 21: /SIDSI/gcgcdata/geneseq/geneseq/AA2000.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	5	15	R45382
2	27	100.0	5	15	R45384
3	27	100.0	5	15	R45386
4	27	100.0	5	15	R45387
5	27	100.0	5	16	R82387
6	27	100.0	5	15	R62389
7	27	100.0	5	18	W33057
8	27	100.0	5	18	W33055
9	27	100.0	5	19	W41099
10	27	100.0	5	19	W41101
11	27	100.0	5	19	W41109
12	27	100.0	5	19	W41240

13	27	100.0	5	19	W41243	Alpha-v-beta-5 ant
14	27	100.0	5	19	W41247	Alpha-v-beta-5 ant
15	27	100.0	5	20	W92307	Cyclic azapeptide
16	24	88.9	5	20	W92302	Cyclic adhesion in
17	24	88.9	5	20	W92306	Cyclic adhesion in
18	23	85.2	4	12	R10408	Fibrinogen recepto
19	23	85.2	4	13	R25316	Cell contact inhib
20	23	85.2	4	14	R32385	Fibrinogen recepto
21	23	85.2	4	14	R69333	Gp IIb/IIIa recept
22	23	85.2	4	15	R54528	Platelet aggregati
23	23	85.2	4	15	R49800	Sequence of peptid
24	23	85.2	4	15	R42568	Trl-/tetra-cyclic
25	23	85.2	4	18	W25179	Rgd-peptide capabl
26	23	85.2	4	19	W52096	Targetting peptide
27	23	85.2	4	19	W50599	GPIIb/IIIa recepto
28	23	85.2	5	12	R10179	RGD-contg. peptide
29	23	85.2	5	12	R11760	Peptide #4 having
30	23	85.2	5	13	R24515	Platelet antagonis
31	23	85.2	5	18	Y08052	Biotin derivative
32	23	85.2	5	18	W33357	Cyclic integrin an
33	23	85.2	5	18	W33358	Cyclic integrin an
34	23	85.2	5	18	W33359	Cyclic integrin an
35	23	85.2	5	18	W33355	Cyclic integrin an
36	23	85.2	5	18	W33356	Cyclic integrin an
37	23	85.2	5	18	W33357	Cyclic integrin an
38	23	85.2	5	18	W33353	Cyclic integrin an
39	23	85.2	5	18	W33354	Cyclic integrin an
40	23	85.2	5	18	W33352	Cyclic integrin an
41	23	85.2	5	18	W33356	Cyclic integrin an
42	23	85.2	5	18	W33160	Integrin inhibiti
43	23	85.2	5	19	W41126	Cyclic peptide 112
44	23	85.2	5	19	W41246	Alpha-v-beta-5 ant
45	23	85.2	5	20	Y43231	RGD-containing pep

#### ALIGNMENTS

RESULT	ID	Key	Location/Qualifiers
1	R45382	Modified-site	1
2	R45382	Modified-site	1
3	R45382	Modified-site	1
4	R45382	Modified-site	1
5	R45382	Modified-site	1
6	R45382	Modified-site	1
7	R45382	Modified-site	1
8	R45382	Modified-site	1
9	R45382	Modified-site	1
10	R45382	Modified-site	1
11	R45382	Modified-site	1
12	R45382	Modified-site	1
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14	R45382	Modified-site	1
15	R45382	Modified-site	1
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19	R45382	Modified-site	1
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38	R45382	Modified-site	1
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40	R45382	Modified-site	1
41	R45382	Modified-site	1
42	R45382	Modified-site	1
43	R45382	Modified-site	1
44	R45382	Modified-site	1
45	R45382	Modified-site	1

XX Cheresh DA, Diefenbach B, Felding-Habermann B, Gurrath M;  
 PI Holzemann G, Jonczyk A, Kessler H, Melzer G, Mueller G;  
 DR WPI: 1994-009982/02.  
 XX  
 PT Compsn. contg. cyclopenta- or hexa-peptide - inhibits adhesion of  
 PT animal cells, used in the treatment and prophylaxis of e.g.  
 PT thrombosis, tumours, osteoporosis or inflammation  
 PS  
 PS Claim 1; Page 7; 9pp; English.  
 XX  
 CC The sequences given in R45370-87 are cyclopenta- and  
 CC cyclohexapeptides which act to inhibit adhesion between animal cells.  
 CC A composition containing these peptides may be used in the  
 CC treatment and prophylaxis of thrombosis, myocardial infarction,  
 CC apoplexy, arteriosclerosis, inflammation, angina pectoris,  
 CC osteoporosis and/or tumour. They are used to induce an adhesion-  
 CC receptor antagonist effect in the subject, to inhibit cell adhesion,  
 CC and in the formation of osteoclasts. They may also be used in wound  
 CC healing compositions and to block beta-3 integrin fibrogen binding.

XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDFV 5  
 |||||  
 Db 1 rgdfv 5

# RESULT 2

ID R45384 standard; Protein; 5 AA.

AC R45384;

DT 06-JUL-1994 (first entry)

DE Cell adhesion inhibition peptide (o).

KW Cyclopentapeptide; cyclohexapeptide; inhibition; adhesion;

KW animal; somatic; cell; thrombosis; myocardial infarction;

KW apoplexy; arteriosclerosis; inflammation; angina pectoris;

KW osteoporosis; tumour; adhesion-receptor antagonist; osteoclast;

KW wound healing; beta-3 integrin; fibrogen binding.

OS Synthetic.

FT Key Location/Qualifiers

FT Modified-site 1 /note= "Amide linkage to Val5 forming a cyclic peptide"

FT Misc-difference 4 /note= "D-form residue"

FT Modified-site 5 /note= "Amide linkage to Arg1 forming a cyclic peptide"

XX EP578083-A.

XX 12-JAN-1994.

XX 26-JUN-1993; 93EP-0110232.

XX 06-JUL-1992; 92US-0909367.

XX 24-FEB-1993; 93US-0022024.

XX (MERE ) MERCK PATENT GMBH.

XX Cheresh DA, Diefenbach B, Felding-Habermann B, Gurrath M;

PI Holzemann G, Jonczyk A, Kessler H, Melzer G, Mueller G;

XX WPI: 1994-009982/02.  
 XX  
 PT Compsn. contg. cyclopenta- or hexa-peptide - inhibits adhesion of  
 PT animal cells, used in the treatment and prophylaxis of e.g.  
 PT thrombosis, tumours, osteoporosis or inflammation  
 PS  
 PS Claim 1; Page 7; 9pp; English.  
 XX  
 CC The sequences given in R45370-87 are cyclopenta- and  
 CC cyclohexapeptides which act to inhibit adhesion between animal cells.  
 CC A composition containing these peptides may be used in the  
 CC treatment and prophylaxis of thrombosis, myocardial infarction,  
 CC apoplexy, arteriosclerosis, inflammation, angina pectoris,  
 CC osteoporosis and/or tumour. They are used to induce an adhesion-  
 CC receptor antagonist effect in the subject, to inhibit cell adhesion,  
 CC and in the formation of osteoclasts. They may also be used in wound  
 CC healing compositions and to block beta-3 integrin fibrogen binding.

XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDFV 5  
 |||||  
 Db 1 rgdfv 5

# RESULT 3

ID R45386 standard; Protein; 5 AA.

AC R45386;

DT 06-JUL-1994 (first entry)

DE Cell adhesion inhibition peptide (q).

KW Cyclopentapeptide; cyclohexapeptide; inhibition; adhesion;

KW animal; somatic; cell; thrombosis; myocardial infarction;

KW apoplexy; arteriosclerosis; inflammation; angina pectoris;

KW osteoporosis; tumour; adhesion-receptor antagonist; osteoclast;

KW wound healing; beta-3 integrin; fibrogen binding.

OS Synthetic.

FT Key Location/Qualifiers

FT Modified-site 1 /note= "Amide linkage to Val5 forming a cyclic peptide"

FT Modified-site 5 /note= "D-form residue, amide linkage to Arg1 forming a cyclic peptide"

XX EP578083-A.

XX 12-JAN-1994.

XX 26-JUN-1993; 93EP-0110232.

XX 06-JUL-1992; 92US-0909367.

XX 24-FEB-1993; 93US-0022024.

XX (MERE ) MERCK PATENT GMBH.

XX Cheresh DA, Diefenbach B, Felding-Habermann B, Gurrath M;

PI Holzemann G, Jonczyk A, Kessler H, Melzer G, Mueller G;

XX WPI: 1994-009982/02.

XX Compsn. contg. cyclopenta- or hexa-peptide - inhibits adhesion of

PT animal cells, used in the treatment and prophylaxis of e.g.  
 PT thrombosis, tumours, osteoporosis or inflammation  
 XX  
 PS Claim 1; Page 7; 9pp; English.  
 CC  
 CC The sequences given in R45370-87 are cyclopenta- and  
 CC cyclohexapeptides which act to inhibit adhesion between animal cells.  
 CC A composition containing these peptides may be used in the  
 CC treatment and prophylaxis of thrombosis, myocardial infarction,  
 CC apllexy, arteriosclerosis, inflammation, angina pectoris,  
 CC osteoporosis and/or tumour. They are used to induce an adhesion-  
 CC receptor antagonist effect in the subject, to inhibit cell adhesion,  
 CC and in the formation of osteoclasts. They may also be used in wound  
 CC healing compositions and to block beta-3 integrin fibrogen binding.  
 CC  
 SO Sequence 5 AA;  
 Query Match 100.0%; Score 27; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 RGDFV 5  
 Db 1 rgdfv 5  
 RESULT 4  
 R45387  
 ID R45387 standard; Protein; 5 AA.  
 AC R45387;  
 XX  
 DT 06-JUL-1994 (first entry)  
 XX  
 DE Cell adhesion inhibition peptide (r).  
 XX  
 KW Cyclopentapeptide; cyclohexapeptide; inhibition; adhesion;  
 KW animal; somatic; cell; thrombosis; myocardial infarction;  
 KW apllexy; arteriosclerosis; inflammation; angina pectoris;  
 KW osteoporosis; tumour; adhesion-receptor antagonist; osteoclast;  
 KW wound healing; beta-3 integrin; fibrogen binding.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note- "Amide linkage to Val5 forming a cyclic peptide"  
 FT MISC-difference 3 /note- "D-form residue"  
 FT Modified-site 5 /note- "Amide linkage to Arg1 forming a cyclic peptide"  
 FT  
 XX  
 PN EP578083-A.  
 XX  
 PD 12-JAN-1994.  
 XX  
 PE 26-JUN-1993; 93EP-0110232.  
 XX  
 PR 06-JUL-1992; 92US-0909367.  
 PR 24-FEB-1993; 93US-0022024.  
 XX  
 PA (MERE ) MERCK PATENT GMBH.  
 XX  
 PI Cheresch DA, Diefenbach B, Felding-Habermann B, Gurrath M;  
 PI Hoeslitzmann G, Jonczyk A, Kessler H, Melzer G, Mueller G;  
 DR WPI; 1994-009982/02.  
 XX  
 PT Compsn. contg. cyclopenta- or hexa-peptide - inhibits adhesion of  
 PT animal cells, used in the treatment and prophylaxis of e.g.  
 PT thrombosis, tumours, osteoporosis or inflammation  
 XX

PS Claim 1; Page 7; 9pp; English.  
 XX  
 CC The sequences given in R45370-87 are cyclopenta- and  
 CC cyclohexapeptides which act to inhibit adhesion between animal cells.  
 CC A composition containing these peptides may be used in the  
 CC treatment and prophylaxis of thrombosis, myocardial infarction,  
 CC apllexy, arteriosclerosis, inflammation, angina pectoris,  
 CC osteoporosis and/or tumour. They are used to induce an adhesion-  
 CC receptor antagonist effect in the subject, to inhibit cell adhesion,  
 CC and in the formation of osteoclasts. They may also be used in wound  
 CC healing compositions and to block beta-3 integrin fibrogen binding.  
 CC  
 SO Sequence 5 AA;  
 Query Match 100.0%; Score 27; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 RGDFV 5  
 Db 1 rgdfv 5  
 RESULT 5  
 R82387  
 ID R82387 standard; peptide; 5 AA.  
 AC R82387;  
 XX  
 DT 03-MAY-1996 (first entry)  
 XX  
 DE Cyclic integrin alpha-v-beta-3 inhibitor peptide no. 62184.  
 XX  
 KW Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;  
 KW fibrinogen; inflammation; apoptosis; restenosis; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 PN W09525543-A1.  
 XX  
 PD 28-SEP-1995.  
 XX  
 PE 09-MAR-1995; 95WO-US03035.  
 XX  
 PR 30-DEC-1994; 94US-036665.  
 PR 18-MAR-1994; 94US-0210715.  
 XX  
 PA (SCRI ) SCRIpps RES INST.  
 XX  
 PI Brooks P, Cheresch DA;  
 DR WPI; 1995-344463/44.  
 XX  
 PT Inhibition of angiogenesis in a tissue, e.g. following angioplasty  
 PT by admin. of a compsn. comprising an alpha-v-beta-3 antagonist,  
 PT useful for regression of established tumours, treating inflamed  
 PT tissue, etc.  
 XX  
 PS Claim 4; Page 47; 135pp; English.  
 XX  
 CC R82386-96 are a group of inhibitor peptides of integrin alpha-v-beta-3.  
 CC The inhibitor peptides may be administered in a compsn. and are useful  
 CC for inhibition of inflamed tissue angiogenesis, e.g. that associated  
 CC with rheumatoid arthritis, retinal angiogenesis associated with  
 CC diabetic retinopathy, that associated with haemangioma, solid  
 CC tumours, or solid tumour metastases. The alpha-v-beta-3 antagonists  
 CC are also useful to induce apoptosis in neovasculture in a tissue.  
 CC The inhibitor peptides are pref. cyclic and contain an RGD sequence.  
 XX  
 SO Sequence 5 AA;

Query Match 100.0%; Score 27; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDV 5  
 11111  
 DB 1 rgdtv 5

RESULT 6  
 R82389.  
 ID R82389 standard; peptide: 5 AA.  
 XX  
 AC R82389;  
 XX  
 DT 03-MAR-1996 (first entry)  
 XX  
 DE Cyclic integrin alpha-v-beta-3 inhibitor peptide no. 62187.  
 XX  
 KW Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;  
 KW fibrinogen; inflammation; apoptosis; restenosis; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT MISC-difference 4 /note="D-Val"  
 FT  
 XX W09525543-A1.  
 XX  
 PD 28-SEP-1995.  
 XX  
 PE 09-MAR-1995; 95WO-US03035.  
 XX  
 PR 30-DEC-1994; 94US-036665.  
 PR 18-MAR-1994; 94US-0210715.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Brooks P, Cheresch DA;  
 XX  
 DR WPI: 1995-344463/44.  
 XX  
 PT Inhibition of angiogenesis in a tissue, e.g. following angioplasty  
 PT - by admin. of a compsn. comprising an alpha-v-beta-3 antagonist;  
 PT useful for regression of established tumours, treating inflamed  
 PT tissue, etc.  
 XX  
 PS Claim 4; Page 47; 135pp; English.  
 PS  
 XX R82386-96 are a group of inhibitor peptides of integrin alpha-v-beta-3.  
 CC The inhibitor peptides may be administered in a compsn. and are useful  
 CC for inhibition of inflamed tissue angiogenesis, e.g. that associated  
 CC with rheumatoid arthritis, retinal angiogenesis associated with  
 CC diabetic retinopathy, that associated with haemangioma, solid  
 CC tumours, or solid tumour metastases. The alpha-v-beta-3 antagonists  
 CC are also useful to induce apoptosis in neovasculture in a tissue.  
 CC The inhibitor peptides are pref. cyclic and contain an RGD sequence.  
 XX  
 SO Sequence 5 AA:

Query Match 100.0%; Score 27; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDV 5  
 11111  
 DB 1 rgdtv 5

RESULT 7  
 W33057

ID W33057 standard; peptide: 5 AA.  
 XX  
 AC W33057;  
 XX  
 DT 26-JAN-1998 (first entry)  
 XX  
 DE Alpha-v, beta-5 vitronectin receptor antagonist.  
 XX  
 KW RGD containing peptide; antagonist; alpha-v, beta-5;  
 KW vitronectin receptor; inhibition; angiogenesis; inflammation;  
 KW rheumatoid arthritis; eye disease; diabetic retinopathy;  
 KW age related macular degeneration; ocular histoplasmosis;  
 KW retinopathy; prematurity; neovascular glaucoma;  
 KW corneal neovascular disorder; transplantation; herpetic; lentic;  
 KW keratitis; pterygium; neovascular pannus; haemangioma;  
 KW solid tumour; metastasis; cytokine; low toxicity;  
 KW vascular endothelial growth factor;  
 KW transforming growth factor alpha; epidermal growth factor; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT MISC-difference 5 /note="D-form residue"  
 FT  
 XX W09706791-A1.  
 XX  
 PD 27-FEB-1997.  
 XX  
 PE 13-AUG-1996; 96WO-US13194.  
 XX  
 PR 14-AUG-1995; 95US-0514799.  
 PR 14-AUG-1996; 96ZA-0006886.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Brooks P, Cheresch DA, Friedlander M;  
 XX  
 DR WPI: 1997-155019/15.  
 XX  
 PT Inhibiting angiogenesis with an antagonist selective for the  
 PT alpha-v,beta-5 integrin receptor - e.g. antibody, RGD peptide or  
 PT organic mimetic, for treatment of inflammation, eye disease, tumours  
 PT etc.  
 XX  
 PS Claim 5; Page 105; 126pp; English.  
 PS  
 XX The present RGD containing peptide is an antagonist of the alpha-v,  
 CC beta-5 vitronectin receptor, which can be used to inhibit  
 CC angiogenesis in alpha-v, beta-5 containing tissue, specifically  
 CC angiogenesis as a result of inflammation (especially rheumatoid  
 CC arthritis), eye disease (especially diabetic retinopathy, age  
 CC related macular degeneration), ocular histoplasmosis, retinopathy of  
 CC prematurity or neovascular glaucoma), corneal neovascular disorders  
 CC (especially transplantation, herpetic or lentic keratitis,  
 CC pterygium and neovascular pannus associated with wearing contact  
 CC lenses), haemangioma, solid tumours and their metastases or  
 CC cytokines (especially vascular endothelial growth factor,  
 CC transforming growth factor alpha or epidermal growth factor). The  
 CC antagonist has the advantage of being very specific, affecting no  
 CC processes other than angiogenesis and therefore of relatively low  
 CC toxicity.  
 XX  
 SO Sequence 5 AA:

Query Match 100.0%; Score 27; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDV 5  
 11111  
 DB 1 rgdtv 5



RESULT 8  
 W33055  
 ID W33055 standard; peptide; 5 AA.  
 AC W33055;  
 DT 26-JAN-1998 (first entry)  
 XX  
 DE Alpha-v, beta-5 vitronectin receptor antagonist.  
 XX  
 KW RGD containing peptide; antagonist; alpha-v, beta-5;  
 KW vitronectin receptor; inhibition; angiogenesis; inflammation;  
 KW rheumatoid arthritis; eye disease; diabetic retinopathy;  
 KW age related macular degeneration; ocular histoplasmosis;  
 KW retinopathy; prematurity; neovascular glaucoma;  
 KW corneal neovascular disorder; transplantation; herpetic; lentic;  
 KW keratitis; pterygium; neovascular pannus; haemangioma;  
 KW solid tumour; metastasis; cytokine; low toxicity;  
 KW vascular endothelial growth factor;  
 KW transforming growth factor alpha; epidermal growth factor; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 4 /note= "D-form residue"  
 XX  
 PN W09706791-A1.  
 XX  
 PD 27-FEB-1997.  
 XX  
 PE 13-AUG-1996; 96WO-US13194.  
 XX  
 PR 14-AUG-1995; 95US-0514799.  
 PR 14-AUG-1996; 96ZA-0006886.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Brooks P, Cheresch DA, Friedlander M;  
 DR WPI; 1997-165019/15.  
 XX  
 PT Inhibiting angiogenesis with an antagonist selective for the  
 PT alpha-v,beta-5 integrin receptor - e.g. antibody, RGD peptide or  
 PT organic mimetic, for treatment of inflammation, eye disease, tumours  
 PT etc.  
 XX  
 PS Claim 5; Page 105; 126pp; English.  
 XX  
 CC The present RGD containing peptide is an antagonist of the alpha-v,  
 CC beta-5 vitronectin receptor, which can be used to inhibit  
 CC angiogenesis in alpha-v, beta-5 containing tissue, specifically  
 CC angiogenesis as a result of inflammation (especially rheumatoid  
 CC arthritis), eye disease (especially diabetic retinopathy, age  
 CC related macular degeneration, ocular histoplasmosis, retinopathy of  
 CC prematurity or neovascular glaucoma), corneal neovascular disorders  
 CC (especially transplantation, herpetic or lentic keratitis,  
 CC pterygium and neovascular pannus associated with wearing contact  
 CC lenses), haemangioma, solid tumours and their metastases or  
 CC cytokines (especially vascular endothelial growth factor,  
 CC transforming growth factor alpha or epidermal growth factor). The  
 CC antagonist has the advantage of being very specific, affecting no  
 CC processes other than angiogenesis and therefore of relatively low  
 CC toxicity.  
 CC  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDFF 5  
 DB 1 rgtff 5  
 RESULT 9  
 W41099  
 ID W41099 standard; Peptide; 5 AA.  
 AC W41099;  
 DT 08-JUN-1998 (first entry)  
 XX  
 DE Alpha-v beta-3 antagonist cyclic peptide 62184 (66203).  
 XX  
 KW Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;  
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;  
 KW diabetic retinopathy; macular degeneration; restenosis; therapy;  
 KW circular; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 4 /note= "D-form residue"  
 XX  
 PN W09745137-A1.  
 XX  
 PD 04-DEC-1997.  
 XX  
 PE 30-MAY-1997; 97WO-US09158.  
 XX  
 PR 31-MAY-1996; 96US-0018733.  
 PR 31-MAY-1996; 96US-0015869.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Brooks P, Cheresch DA;  
 DR WPI; 1998-032334/03.  
 XX  
 PT Packaging material containing polypeptide antagonist of alphav,  
 PT beta3 integrin - used for inhibition of angiogenesis, and for  
 PT treating tumours, inflammation, eye diseases etc.  
 XX  
 PS Example 1; Page 48; 234pp; English.  
 XX  
 CC This synthetic RGD-containing cyclic peptide, designated 62184 or  
 CC 66203, is a particularly preferred peptide that has integrin  
 CC alpha-v beta3 antagonist activity. It exhibits preferential  
 CC inhibition of fibrinogen binding to the alpha-v beta-3 receptor.  
 CC It can be prepared using standard solid-phase synthesis  
 CC techniques. The invention relates to the discovery that  
 CC angiogenesis is mediated by the specific vitronectin receptor  
 CC alpha-v beta-3, and that inhibition of alpha-v beta-3 function  
 CC inhibits angiogenesis. Claimed antagonists of alpha-v beta-3  
 CC comprise C-terminal fragments (see W41083-94) of human or chicken  
 CC matrix metalloproteinase-2, fusion polypeptides, cyclic or linear  
 CC polypeptides, derivatised polypeptides, a monoclonal antibody or  
 CC organic mimetic compound. They can be used to inhibit angiogenesis  
 CC in inflamed tissue (for treatment of arthritis or rheumatoid  
 CC arthritis), in solid tumours or metastases (particularly to induce  
 CC regression or inhibit tumour growth), and in ocular disorders such  
 CC as diabetic retinopathy and macular degeneration, as well as to  
 CC treat restenosis (all claimed).  
 CC  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDV 5  
 |||||  
 Db 1 rgdtv 5

## RESULT 10

W41101  
 ID W41101 standard; Peptide; 5 AA.  
 AC W41101;

DT 08-JUN-1998 (first entry)

DE Alpha-v beta-3 antagonist cyclic peptide 62187.

XX Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;  
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;  
 KW diabetic retinopathy; macular degeneration; restenosis; therapy;  
 KW circular; cyclic.

XX Synthetic.

OS Key Location/Qualifiers

FH Key Misc-difference 5 /note="D-form residue"

FT W09745137-A1.

XX 04-DEC-1997.

PF 30-MAY-1997; 97WO-US09158.

XX 31-MAY-1996; 96US-0018733.

PR 31-MAY-1996; 96US-0015869.

XX (SCRI ) SCRIPPS RES INST.

PA Brooks P, Cheres DA;

PI WPI: 1998-032334/03.

XX Packaging material containing polypeptide antagonist of alphav,  
 PT betas3 integrin - used for inhibition of angiogenesis, and for  
 PT treating tumours, inflammation, eye diseases etc.

XX Example 1; Page 48; 234pp; English.

XX This synthetic RGD-containing cyclic peptide, designated 62187,  
 CC is a particularly preferred peptide that has integrin  
 CC alpha-v beta-3 antagonist activity. It exhibits preferential  
 CC inhibition of fibrinogen binding to the alpha-v beta-3 receptor.  
 CC It can be prepared using standard solid-phase synthesis  
 CC techniques. The invention relates to the discovery that  
 CC angiogenesis is mediated by the specific vitronectin receptor  
 CC alpha-v beta-3, and that inhibition of alpha-v beta-3 function  
 CC inhibits angiogenesis. Claimed antagonists of alpha-v beta-3  
 CC comprise C-terminal fragments (see W41083-94) of human or chicken  
 CC matrix metalloproteinase-2, fusion polypeptides, cyclic or linear  
 CC polypeptides, derivatised polypeptides, a monoclonal antibody or  
 CC organic mimetic compound. They can be used to inhibit angiogenesis  
 CC in inflamed tissue (for treatment of arthritis or rheumatoid  
 CC arthritis), in solid tumours or metastases (particularly to induce  
 CC regression or inhibit tumour growth), and in ocular disorders such  
 CC as diabetic retinopathy and macular degeneration, as well as to  
 CC treat restenosis (all claimed).

XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDV 5  
 |||||  
 Db 1 rgdtv 5

## RESULT 11

W41109  
 ID W41109 standard; Peptide; 5 AA.  
 AC W41109;

DT 08-JUN-1998 (first entry)

DE Alpha-v beta-3 antagonist cyclic peptide 121974 (85189).

XX Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;  
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;  
 KW diabetic retinopathy; macular degeneration; restenosis; therapy;  
 KW circular; cyclic.

XX Synthetic.

OS Key Location/Qualifiers

FH Key Modified-site 5 /note="valine residue NH2 terminal is  
 FT methylated"

FT W09745137-A1.

XX 04-DEC-1997.

PF 30-MAY-1997; 97WO-US09158.

XX 31-MAY-1996; 96US-0018733.

PR 31-MAY-1996; 96US-0015869.

XX (SCRI ) SCRIPPS RES INST.

PA Brooks P, Cheres DA;

PI WPI: 1998-032334/03.

XX Packaging material containing polypeptide antagonist of alphav,  
 PT betas3 integrin - used for inhibition of angiogenesis, and for  
 PT treating tumours, inflammation, eye diseases etc.

XX Example 1; Page 51; 234pp; English.

XX This synthetic RGD-containing cyclic peptide, designated 121974 or  
 CC 85189, is a particularly preferred peptide that has integrin  
 CC alpha-v beta-3 antagonist activity. It can be prepared using  
 CC standard solid-phase synthesis techniques. The invention relates  
 CC to the discovery that angiogenesis is mediated by the specific  
 CC vitronectin receptor alpha-v beta-3, and that inhibition of alpha-v  
 CC beta-3 function inhibits angiogenesis. Claimed antagonists of  
 CC alpha-v beta-3 comprise C-terminal fragments (see W41083-94) of  
 CC human or chicken matrix metalloproteinase-2, fusion polypeptides,  
 CC cyclic or linear polypeptides, derivatised polypeptides, a  
 CC monoclonal antibody or organic mimetic compound. They can be used  
 CC to inhibit angiogenesis in inflamed tissue (for treatment of  
 CC arthritis or rheumatoid arthritis), in solid tumours or metastases  
 CC (particularly to induce regression or inhibit tumour growth), and  
 CC in ocular disorders such as diabetic retinopathy and macular  
 CC degeneration, as well as to treat restenosis (all claimed).

XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDFV 5  
| | | | |  
Db 1 rgdfv 5

## RESULT 12

W41240  
ID W41240 standard; protein; 5 AA.

XX W41240;

AC W41240;

XX 09-JUN-1998 (first entry)

XX Alpha-v-beta-5 antagonistic peptide 62184.

XX Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;

XX angiogenesis; tumour growth; restenosis; neovascularisation.

XX Synthetic.

XX Key Location/Qualifiers

XX MISC-difference 1..5 /note- "peptide is made cyclic via the first and

XX MISC-difference 4 /note- "D-form residue"

XX W09745447-A1.

XX 04-DEC-1997.

XX 30-MAY-1997; 97MO-US09099.

XX 31-MAY-1996; 96US-0018733.

XX 31-MAY-1996; 96US-0015869.

XX (SCRI ) SCRIIPS RES INST.

XX Brooks P, Cheresh DA, Friedlander M;

XX WPI; 1998-041758/04.

XX WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav,

XX betas integrin - used for inhibition of angiogenesis, and for

XX treating tumours, inflammation, eye diseases etc.

XX Disclosure; Page 41; 117pp; English.

XX The present peptide represents an alpha-v-beta-5 integrin antagonists.

XX Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5

XX can inhibit angiogenesis. The specification describes a novel

XX labelled package that contains an inhibitor of angiogenesis i.e. an

XX alpha-v-beta-5 antagonising polypeptide that binds to integrin

XX alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.

XX The antagonists are used to inhibit angiogenesis in inflamed tissue, in

XX solid tumours or metastases, and in a wide range of ocular disorders

XX (e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or

XX corneal transplants). They are particularly used to induce regression or

XX to inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be

XX used to treat restenosis caused by migration of smooth muscle cells

XX following angioplasty and to reduce blood supply to selected tissues.

XX The antagonists particularly inhibit neovascularisation where this is

XX induced by cytokines, e.g. transforming growth factor alpha, epidermal

XX growth factor or especially vascular endothelial growth factor.

XX note: this sequence does not appear in the specification; it was created

XX using information provided.

XX Sequence 5 AA;

XX SQ

XX

XX

XX

XX

XX

QY 1 RGDFV 5  
| | | | |  
Db 1 rgdfv 5

## RESULT 13

W41243  
ID W41243 standard; protein; 5 AA.

XX W41243;

XX 09-JUN-1998 (first entry)

XX Alpha-v-beta-5 antagonistic peptide 62187.

XX Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;

XX angiogenesis; tumour growth; restenosis; neovascularisation.

XX Synthetic.

XX Key Location/Qualifiers

XX MISC-difference 1..5 /note- "peptide is made cyclic via the first and

XX MISC-difference 5 /note- "D-form residue"

XX W09745447-A1.

XX 04-DEC-1997.

XX 30-MAY-1997; 97MO-US09099.

XX 31-MAY-1996; 96US-0018733.

XX 31-MAY-1996; 96US-0015869.

XX (SCRI ) SCRIIPS RES INST.

XX Brooks P, Cheresh DA, Friedlander M;

XX WPI; 1998-041758/04.

XX WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav,

XX betas integrin - used for inhibition of angiogenesis, and for

XX treating tumours, inflammation, eye diseases etc.

XX Disclosure; Page 41; 117pp; English.

XX The present peptide represents an alpha-v-beta-5 integrin antagonists.

XX Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5

XX can inhibit angiogenesis. The specification describes a novel

XX labelled package that contains an inhibitor of angiogenesis i.e. an

XX alpha-v-beta-5 antagonising polypeptide that binds to integrin

XX alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.

XX The antagonists are used to inhibit angiogenesis in inflamed tissue, in

XX solid tumours or metastases, and in a wide range of ocular disorders

XX (e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or

XX corneal transplants). They are particularly used to induce regression or

XX to inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be

XX used to treat restenosis caused by migration of smooth muscle cells

XX following angioplasty and to reduce blood supply to selected tissues.

XX The antagonists particularly inhibit neovascularisation where this is

XX induced by cytokines, e.g. transforming growth factor alpha, epidermal

XX growth factor or especially vascular endothelial growth factor.

XX note: this sequence does not appear in the specification; it was created

XX using information provided.

XX Sequence 5 AA;

XX SQ

XX

XX

XX

XX

XX

Query Match 100.0%; Score 27; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 27; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGDFV 5  
 |||||  
 Db 1 rgdtv 5

RESULT 14  
 ID W41247 standard; protein; 5 AA.

XX W41247;

DT 09-JUN-1998 (first entry)

DE Alpha-v-beta-5 antagonistic peptide.

KW Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;  
 KM angiogenesis; tumour growth; restenosis; neovascularisation.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 4 /note="D-form residue"

PN W09745447-A1.

PD 04-DEC-1997.

PE 30-MAY-1997; 97WO-US09099.

PR 31-MAY-1996; 96US-0018733.

PR 31-MAY-1996; 96US-0015869.

PA (SCRI ) SCRIPPS RES INST.

PI Brooks P, Cheresch DA, Friedlander M;

DR WPI: 1998-041758/04.

PT Packaging material containing polypeptide antagonist of alphav,  
 PT betas integrin - used for inhibition of angiogenesis, and for  
 PT treating tumours, inflammation, eye diseases etc.

PS Disclosure; Page 38; 117pp; English.

XX The present peptide represents an alpha-v-beta-5 integrin antagonists.

CC Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5  
 CC can inhibit angiogenesis. The specification describes a novel

CC labelled package that contains an inhibitor of angiogenesis i.e. an  
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin

CC alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.

CC The antagonists are used to inhibit angiogenesis in inflamed tissue, in  
 CC solid tumours or metastases, and in a wide range of ocular disorders

CC (e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or  
 CC corneal transplants). They are particularly used to induce regression or

CC used to treat restenosis caused by migration of smooth muscle cells

CC following angioplasty and to reduce blood supply to selected tissues.

CC The antagonists particularly inhibit neovascularisation where this is  
 CC induced by cytokines, e.g. transforming growth factor alpha, epidermal

CC growth factor or especially vascular endothelial growth factor.

CC note: this sequence does not appear in the specification; it was created  
 CC using information provided.

XX Sequence 5 AA;

XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 19; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDFV 5  
 |||||  
 Db 1 rgdtv 5

RESULT 15  
 ID W92307 standard; peptide; 5 AA.

XX W92307;

DT 01-APR-1999 (first entry)

DE Cyclic azapeptide #1.

KW Cyclic peptide; azapeptide; integrin inhibitor; treatment; thrombosis;  
 KM cardiac infarct; coronary heart disease; arteriosclerosis; tumour;

KW osteoporosis; inflammation; infection; angiogenesis; antimicrobial;

KW diagnosis; platelet metabolism; fibrinogen receptor; cancer; metastasis;  
 KM intracellular signalling; GpIb/IIIa receptor; matrix metalloproteinase;

KM vitronectin receptor.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 1..5 /note="The carboxy group of Val(5) is condensed onto  
 FT the amino group of Arg(1) to form a cyclic  
 FT peptide. Not true N- and C- terminus.  
 FT Val(5) can be modified by N-Me"

FT Modified-site 2 /note="aza-gly"

FT Misc-difference 4 /note="can be D-form residue"

FT Misc-difference 5 /note="can be D-form residue"

PN DE19728524-A1.

PD 07-JAN-1999.

PE 04-JUL-1997; 97DE-1028524.

PR 04-JUL-1997; 97DE-1028524.

PA (MERE ) MERCK PATENT GMBH.

PI Goodman SL, Janczyk A, Kessler H, Schmitt J, Wermuth J;

DR WPI: 1999-072017/07.

PT New cyclic peptide(s) containing aza-amino acid - are  
 PT inhibitors of integrin-ligand interaction, used to treat e.g.  
 PT thrombosis, cardiac infarct, coronary heart disease and tumours

PS Claim 3a; Page 11; 12pp; German.

XX This invention is concerned with novel cyclic peptides of formula

CC cyclo(aArg-Gly-aaSP-ax-ax) where aArg = Arg or aza-Arg, aGly = Gly or  
 CC aza-Gly, aaSP = Asp or aza-Asp, ax, ax = Ala, Asn, Asp, Arg, Cys, Gln,

CC Glu, Gly, His, Ile, Leu, Lys, Met, Nle (norleucine), Orn (ornithine),  
 CC Phe, Phg (phenylglycine), Pro, Ser, Thr, Tic (tetrahydroisouquinoline-

CC 3-carboxylic acid), Trp, Tyr, Val or NH-Q-CO, or the corresponding  
 CC aza-amino acids, O = 1-6C alkylene, at least one amino acid (aa) in the

CC peptide has the alpha-carbon atom replaced by nitrogen also the aa may  
 CC be derivatised and are coupled together by peptide bonds and optically

CC active amino acids may be in D- or L-forms. The peptides are integrin  
 CC inhibitors, specifically for treating and preventing thrombosis, cardiac

CC infarct, coronary heart disease, arteriosclerosis, tumours, osteoporosis,  
 CC inflammation and infections, or generally any disease where angiogenesis

CC is involved, in human or veterinary medicine. The peptides also have  
 CC antimicrobial activity, are used for diagnosis and location of thrombi,  
 CC and for studying metabolism of platelets at different stages of

CC activation or intracellular signalling mechanisms of the fibrinogen  
CC receptor, and for affinity purification of integrins. The peptides  
CC inhibit interaction between the alpha v, beta 3 and beta 5 receptors with  
CC their ligands, e.g. they prevent binding of fibrinogen to the GpIIb/IIIa  
CC receptor, thus preventing metastatic spread of cancers, and prevent  
CC binding of matrix metalloproteinase to the vitronectin (alpha v beta 3)  
CC receptor. This sequence is a specific claimed example of a novel peptide  
CC of the invention.  
XX

SQ Sequence 5 AA:

Query Match 100.0%; Score 27; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDV 5  
|||  
|||  
DB 1 rgdtv 5

Search completed: March 6, 2001, 09:45:52  
Job time: 58 sec

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OM protein - protein search, using sw model

Run on: March 6, 2001, 09:45:18 ; Search time 19.1 Seconds  
(without alignments)  
4.701 Million cell updates/sec

Title: US-09-081-522-7

Perfect score: 27

Sequence: 1 RGDV 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 14061

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6.COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/PTUS.COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	5	1	US-08-210-715-5 Sequence 5, Appl
2	27	100.0	5	1	US-08-210-715-7 Sequence 7, Appl
3	27	100.0	5	1	US-08-366-665-5 Sequence 5, Appl
4	27	100.0	5	1	US-08-366-665-7 Sequence 7, Appl
5	27	100.0	5	2	US-08-616-770-2 Sequence 2, Appl
6	23	85.2	4	1	US-07-932-200-10 Sequence 10, Appl
7	23	85.2	4	1	US-08-536-116A-68 Sequence 68, Appl
8	23	85.2	4	2	US-08-668-871-12 Sequence 12, Appl
9	23	85.2	4	2	US-08-669-683-12 Sequence 12, Appl
10	23	85.2	4	2	US-08-387-749-10 Sequence 10, Appl
11	23	85.2	4	2	US-08-335-832-25 Sequence 25, Appl
12	23	85.2	4	2	US-08-753-781-20 Sequence 28, Appl
13	23	85.2	4	2	US-08-361-864-28 Sequence 28, Appl
14	23	85.2	4	4	PT-US93-08231-10 Patent No. 5330911
15	23	85.2	4	5	US-08-315-026B-10 Patent No. 5330911
16	23	85.2	5	2	US-08-616-770-1 Sequence 10, Appl
17	23	85.2	5	2	US-08-754-773B-10 Sequence 10, Appl
18	23	85.2	5	3	US-09-141-127-23 Sequence 23, Appl
19	23	85.2	5	3	US-09-155-721-1 Sequence 1, Appl
20	23	85.2	5	3	US-09-155-721-1 Sequence 1, Appl
21	23	85.2	5	3	US-09-155-721-2 Sequence 2, Appl
22	23	85.2	5	3	US-09-155-721-4 Sequence 4, Appl
23	23	85.2	5	3	US-09-155-721-5 Sequence 5, Appl
24	23	85.2	5	3	US-09-155-721-6 Sequence 6, Appl
25	23	85.2	5	3	US-09-155-721-7 Sequence 7, Appl
26	23	85.2	5	3	US-09-155-721-8 Sequence 8, Appl
27	23	85.2	5	3	US-09-155-721-9 Sequence 9, Appl
28	23	85.2	5	5	Patent No. 5330911

29	22	81.5	5	3	US-08-694-387A-22 Sequence 22, Appl
30	22	81.5	5	3	US-08-694-387A-23 Sequence 23, Appl
31	22	81.5	5	3	US-08-694-387A-24 Sequence 24, Appl
32	22	81.5	5	3	US-08-694-387A-25 Sequence 25, Appl
33	22	81.5	5	3	US-08-694-387A-27 Sequence 27, Appl
34	22	81.5	5	3	US-08-694-387A-29 Sequence 29, Appl
35	22	81.5	5	3	US-08-694-387A-30 Sequence 30, Appl
36	22	81.5	5	3	US-08-694-387A-32 Sequence 32, Appl
37	22	81.5	5	3	US-08-694-387A-33 Sequence 33, Appl
38	22	81.5	5	3	US-08-694-387A-34 Sequence 34, Appl
39	22	81.5	5	3	US-08-694-387A-35 Sequence 35, Appl
40	22	81.5	5	3	US-08-694-387A-37 Sequence 37, Appl
41	22	81.5	5	3	US-08-694-387A-38 Sequence 38, Appl
42	22	81.5	5	3	US-08-694-387A-39 Sequence 39, Appl
43	22	81.5	5	3	US-08-694-387A-40 Sequence 40, Appl
44	21	77.8	5	1	US-08-210-715-6 Sequence 6, Appl
45	21	77.8	5	1	US-08-210-715-9 Sequence 9, Appl

## ALIGNMENTS

RESULT 1  
US-08-210-715-5  
Sequence 5, Application US/08210715  
Patent No. 5753230  
GENERAL INFORMATION:  
APPLICANT: Brooks, Peter  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESS: Research Institute  
STREET: 10665 No. 5753230th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/210,715  
FILING DATE: 18-MAR-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 419.0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..5  
OTHER INFORMATION: /label- cyclo  
OTHER INFORMATION: /note- "Cyclo signifies a cyclic peptide; lower  
OTHER INFORMATION: case letters indicate a D-amino acid; capital  
OTHER INFORMATION: letters indicate a L-amino acid."

US-08-210-715-5

Query Match 100.0%; Score 27; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDV 5  
11111  
DB 1 RGDV 5

RESULT 2  
US-08-210-715-7  
Sequence 7, Application US/08210715  
Patent No. 5753230

GENERAL INFORMATION:  
APPLICANT: Brooks, Peter  
APPLICANT: Cheres, David A  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 No. 5753230th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/210.715  
FILING DATE: 18-MAR-1994  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 419.0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..5

OTHER INFORMATION: /label- cyclo  
OTHER INFORMATION: /note- "Cyclo signifies a cyclic peptide; lower  
OTHER INFORMATION: case letters indicate a D-amino acid; capital  
OTHER INFORMATION: letters indicate a L-amino acid."  
US-08-210-715-7

Query Match 100.0%; Score 27; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDV 5  
11111  
DB 1 RGDV 5

RESULT 3  
US-08-366-665-5  
Sequence 5, Application US/08366665  
Patent No. 576591

GENERAL INFORMATION:  
APPLICANT: Brooks, Peter  
APPLICANT: Cheres, David A  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 No. 576591th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/366.665  
FILING DATE: 30-DEC-1994  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/210.715  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 419.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..5

OTHER INFORMATION: /label- cyclo  
OTHER INFORMATION: /note- "Cyclo signifies a cyclic peptide; lower  
OTHER INFORMATION: case letters indicate a D-amino acid; capital  
OTHER INFORMATION: letters indicate a L-amino acid."  
US-08-366-665-5

Query Match 100.0%; Score 27; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDV 5  
11111  
DB 1 RGDV 5

RESULT 4  
US-08-366-665-7  
Sequence 7, Application US/08366665  
Patent No. 576591  
GENERAL INFORMATION:



APPLICANT: Brooks, Peter  
APPLICANT: Chesh, David A  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 No. 576591th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/366,665  
FILING DATE: 30-DEC-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/210,715  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Filling, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 419.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1-5  
OTHER INFORMATION: /label- cyclo  
OTHER INFORMATION: /note- "Cyclo signifies a cyclic peptide; lower  
OTHER INFORMATION: case letters indicate a D-amino acid; capital  
letters indicate a L-amino acid."  
US-08-366-665-7

Query Match 100.0%; Score 27; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDFV 5  
DB 1 RGDFV 5

RESULT 5  
US-08-616-770-2  
Sequence 2, Application US/08616770  
Patent No. 5848692  
GENERAL INFORMATION:  
APPLICANT: Jonczyk, Alfred  
APPLICANT: Holzemann, Gunter  
APPLICANT: Felding-Habermann, Brunhilde  
APPLICANT: Rippmann, Friedrich  
APPLICANT: Diefendach, Beate  
APPLICANT: Kessler, Horst  
APPLICANT: Haubner, Roland

APPLICANT: Westmuth, Jochem  
TITLE OF INVENTION: Cyclic peptides containing Arg-Gly-Asp, and  
TITLE OF INVENTION: Derivatives thereof, as Adhesion Inhibitors  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.  
STREET: 2200 Clarendon Boulevard, Suite 1400  
CITY: Arlington  
STATE: VA  
COUNTRY: U.S.A.  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/616,770  
FILING DATE: 15-MAR-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/220,858  
FILING DATE: 31-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 43 10 643.9  
FILING DATE: 01-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Heaney, Brian P.  
REGISTRATION NUMBER: 32,542  
REFERENCE/DOCKET NUMBER: MERCK 1566C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: circular  
MOLECULE TYPE: peptide  
US-08-616-770-2

Query Match 100.0%; Score 27; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDFV 5  
DB 1 RGDFV 5

RESULT 6  
US-07-932-200-10  
Sequence 10, Application US/07932200  
Patent No. 5368862  
GENERAL INFORMATION:  
APPLICANT: VENTON, DUANE L.  
APPLICANT: HOPFINGER, ANTON J.  
APPLICANT: LE BRETON, GUY  
TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING  
TITLE OF INVENTION: USEFUL PEPTIDES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEWMARK  
STREET: 419 SEVENTH STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/932,200  
FILING DATE: 21-AUG-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, IYER P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: VENTON-1B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3526  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-932-200-10

Query Match 85.2%; Score 23; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDF 4  
1111  
Db 1 RGDF 4

RESULT 7  
US-08-596-116A-68  
Sequence 68, Application US/08596116A  
Patent No. 5721213  
GENERAL INFORMATION:  
APPLICANT: SATO, Yoshimi  
APPLICANT: HAYASHI, Yoshio  
APPLICANT: KATADA, Jun  
TITLE OF INVENTION: No. 5721213el Peptides, Active\*as Inhibitors of  
NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3+ Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: WordPerfect 6.1 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/596,116A  
FILING DATE: 30 JAN 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PC7/JP94/01611  
FILING DATE: 29 SEP 1994  
APPLICATION NUMBER: JP 245541  
FILING DATE: 30 SEP 1993  
APPLICATION NUMBER: JP 50602  
FILING DATE: 22 MAR 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Toffenetti, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 2002/3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-429-1776

TELEFAX: 202-425-0796  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-596-116A-68

Query Match 85.2%; Score 23; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDF 4  
1111  
Db 1 RGDF 4

RESULT 8  
US-08-668-871-12  
Sequence 12, Application US/08668871  
Patent No. 5811389  
GENERAL INFORMATION:  
APPLICANT: Baunwarth, Wilhelm  
APPLICANT: Gerber, Ferdinand  
APPLICANT: Grieder, Alfred  
APPLICANT: Kneizeringer, Andreas  
APPLICANT: Mueller, Klaus  
APPLICANT: Obrecht, Daniel  
TITLE OF INVENTION: TRI- AND TETRACYCLIC COMPOUNDS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07110-1199  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/668,871  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,508  
FILING DATE:  
APPLICATION NUMBER: CH 2725/92  
FILING DATE: 31-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Kass, Alan P.  
REGISTRATION NUMBER: 32142  
REFERENCE/DOCKET NUMBER: RAN 4781/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-4205  
TELEFAX: (201) 235-3500  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-668-871-12

Query Match 85.2%; Score 23; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDF 4  
1111  
Db 1 RGDF 4

RESULT 9  
US-08-669-683-12  
Sequence 12, Application US/08669683  
Patent No. 5811548

GENERAL INFORMATION:  
APPLICANT: Baunwarth, Wilhelm  
APPLICANT: Gerber, Ferdinand  
APPLICANT: Grieder, Alfred  
APPLICANT: Knieringer, Andreas  
APPLICANT: Mueller, Klaus  
APPLICANT: Obrecht, Daniel  
TITLE OF INVENTION: TRI- AND TETRACYCLIC COMPOUNDS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07110-1199

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,683  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,508  
FILING DATE: 31-AUG-1992  
APPLICATION NUMBER: CH 2725/92  
FILING DATE: 31-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Kass, Alan P.  
REGISTRATION NUMBER: 32142  
REFERENCE/DOCKET NUMBER: RAN 4781/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-4205  
TELEFAX: (201) 235-3500  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-669-683-12

Query Match 85.2%; Score 23; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDF 4  
1111  
Db 1 RGDF 4

RESULT 10  
US-08-387-749-10  
Sequence 10, Application US/08387749  
Patent No. 5814460  
GENERAL INFORMATION:  
APPLICANT: VENTON, DUANE L.  
APPLICANT: HOPFINGER, ANTON J.

APPLICANT: LE BRETON, GUY  
TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING  
TITLE OF INVENTION: USEFUL PEPTIDES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 SEVENTH STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/387,749  
FILING DATE: 21-Feb-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08231  
FILING DATE: 09-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/932,200  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/813,315  
FILING DATE: 21-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/00891  
FILING DATE: 14-FEB-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/480,865  
FILING DATE: 14-FEB-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, IVER P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: VENTON-1C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-387-749-10

Query Match 85.2%; Score 23; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDF 4  
1111  
Db 1 RGDF 4

RESULT 11  
US-08-335-832-25  
Sequence 25, Application US/08335832  
Patent No. 5925331  
GENERAL INFORMATION:  
APPLICANT: Dean, Richard T.  
APPLICANT: Lister-James, John  
TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
TITLE OF INVENTION: Tumor Imaging  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.  
STREET: 10 South Wacker Drive Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,832  
FILING DATE: 05-JAN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5925331nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,216-I  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /label-ma  
OTHER INFORMATION: /note- "The amino terminus is modified by covalent  
OTHER INFORMATION: linkage to an mercaptocetyl group."  
US-08-335-832-25

Query Match 85.2%; Score 23; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDF 4  
|||  
DB 1 RGDF 4

RESULT 12  
US-08-753-781-20  
Sequence 20, Application US/08753781C  
GENERAL INFORMATION:  
APPLICANT: Markland Jr., Francis S.  
APPLICANT: Bush, Larry R.  
APPLICANT: Swenson, Stephen  
APPLICANT: Flores Sanchez, Eladio  
TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY  
FILE REFERENCE: DITI 124  
CURRENT APPLICATION NUMBER: US/08/753,781C  
CURRENT FILING DATE: 1996-12-02  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 20  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: meercptocetyl  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:synthetic  
OTHER INFORMATION: peptide

US-08-753-781-20

Query Match 85.2%; Score 23; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDF 4  
|||  
DB 1 RGDF 4

RESULT 13  
US-08-361-864-28  
Sequence 28, Application US/08361864  
Patent No. 5977064  
GENERAL INFORMATION:  
APPLICANT: Dean, Richard T  
APPLICANT: Lister-James, John  
TITLE OF INVENTION: Multimeric Polyvalent Antithrombotic  
TITLE OF INVENTION: Agents  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Allegretti & Witcoff, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,864  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/955,466A  
FILING DATE: 19921002  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5977064nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,668  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-361-864-28

Query Match 85.2%; Score 23; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDF 4  
|||  
DB 1 RGDF 4

RESULT 14  
PCT-US93-08231-10  
Sequence 10, Application PC/TUS9308231  
GENERAL INFORMATION:  
APPLICANT: VENTON, DUANE L.  
APPLICANT: HOPFINGER, ANTON J.

Search completed: March 6, 2001, 09:45:18  
Job time: 25 sec

APPLICANT: LE BRETON, GUY  
TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEWMARK  
STREET: 419 SEVENTH STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08231  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, IVER P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: VENTONIC.PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-08231-10

Query Match 85.2%; Score 23; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDF 4  
|||  
Db 1 RGDF 4

RESULT 15  
5330911-12  
Patent No. 5330911  
APPLICANT: HUBBELL, JEFFREY A.; MASSIA, STEPHEN P.; DESAI,  
NEIL P.  
TITLE OF INVENTION: SURFACES HAVING DESIRABLE CELL  
ADHESIVE EFFECTS  
NUMBER OF SEQUENCES: 27  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/527,198  
FILING DATE: 21-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 414,144  
FILING DATE: 28-SEP-1989  
SEQ ID NO: 12:  
LENGTH: 4  
5330911-12

Query Match 85.2%; Score 23; DB 5; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDF 4  
|||  
Db 1 RGDF 4

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 6, 2001, 09:47:29 ; Search time 20.46 Seconds

(without alignments)  
16.594 Million cell updates/sec

Title: US-09-081-522-7

Perfect score: 27

Sequence: 1 RGFV 5

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 205

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR66:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	44.4	4	2	PT0711
2	12	44.4	5	2	A32516
3	12	44.4	5	2	PQ0689
4	12	44.4	5	2	A44692
5	12	44.4	5	2	B61445
6	12	44.4	5	2	A61445
7	12	44.4	5	2	PT0513
8	12	44.4	5	2	PT0538
9	12	44.4	5	2	PT0703
10	12	44.4	5	2	PT0690
11	12	44.4	5	2	PT0573
12	12	44.4	5	2	PT0679
13	12	44.4	4	1	ECXAA
14	12	44.4	4	2	A25844
15	12	44.4	4	2	S33990
16	12	44.4	4	2	S47552
17	12	44.4	5	2	B61168
18	12	44.4	5	2	PT0525
19	12	44.4	5	2	PT0608
20	12	44.4	5	2	PT0695
21	12	44.4	5	2	PT0700
22	12	44.4	5	2	S68326
23	12	44.4	5	4	A58728
24	12	44.4	5	4	D41654
25	12	44.4	5	2	PT0677
26	12	44.4	5	2	A32014
27	12	44.4	5	2	B45525
28	12	44.4	5	2	PT0540
29	12	44.4	5	2	A23751

30	7	25.3	4	2	ECNK	cardioexcitatory n
31	7	25.9	4	2	S09478	globulin IV alpha
32	7	25.3	4	2	A35779	neuropeptide Antho
33	7	25.3	4	2	A60418	FMRFamide - polych
34	7	25.3	4	2	B53284	T-cell receptor be
35	7	25.9	5	2	PT0308	Ig heavy chain CRD
36	7	25.9	5	2	PT0729	T-cell receptor be
37	6	22.2	3	2	GKHU	growth-modulating
38	6	22.2	3	2	A60898	bursin - chicken
39	6	22.2	3	2	B23751	spinal cord peptid
40	6	22.2	3	2	PT0636	T-cell receptor be
41	6	22.2	3	2	PT0571	T-cell receptor be
42	6	22.2	3	2	S63328	blood cell protein
43	6	22.2	4	2	A32039	tyrosine-melanocyt
44	6	22.2	4	2	PT0140	carbon-monoxide de
45	6	22.2	4	2	A25209	protein-glutamine

#### ALIGNMENTS

RESULT 1

PT0711

T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence-revision 17-Jul-1992 #ext-change 30-May-1997

C:Accession: PT0607; PT0674; PT0678; PT0570; PT0711; PT0710

R:Reaney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions

A:Reference number: PT0509; MUID:91277601

A:Accession: PT0607

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-4 <FE1>

A:Experimental source: newborn thymus, strain BALB/c, 120-2J

A:Accession: PT0678

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-4 <FE2>

A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G

A:Accession: PT0678

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-4 <FE3>

A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L

A:Accession: PT0570

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-4 <FE4>

A:Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I

A:Accession: PT0711

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-4 <FE5>

A:Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)

C:Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GD 3

DB 3 GD 4

RESULT 2

A32516

cholecystokinin-5 - dog

N:Alternate names: CCK-5

C:Species: Canis lupus familiaris (dog)

C>Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 18-Aug-2000  
C/Accession: A32516

R/Shively, J.; Reeve Jr., J.R.; Exselsheim, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.E.  
Am. J. Physiol. 252, G272-G275, 1987

A/Title: CCK-8: sequence analysis of a small cholecystokinin from canine brain and intest

A/Reference number: A32516; MUID:87153871

A/Accession: A32516

A/Molecule type: protein

A/Residues: 1-5 <SH1>

C/Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecysti

C/Superfamily: gastrin

C/Keywords: amidated carboxyl end; neuropeptide

F/5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 44.4%; Score 12; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 DF 4

DB 4 DF 5

RESULT 3

Photosystem I 10.4K H1 chain - common tobacco (fragment)

C/Species: Nicotiana tabacum (common tobacco)

C/Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999

C/Accession: P00689

R/Ohta, N.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.

Plant Physiol. 102, 1259-1267, 1993

A/Title: Molecular heterogeneity of photosystem I. psad, psaf, psah and psal are

A/Reference number: P00689; MUID:94105345

A/Accession: P00689

A/Molecule type: protein

A/Residues: 1-5 <O80>

C/Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 44.4%; Score 12; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GD 3

DB 3 GD 4

RESULT 4

A44692

fulicin - giant African snail

C/Species: Achatina fulica (giant African snail)

C/Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 11-Jul-1997

C/Accession: A44692

R/Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; No

Biochem. Biophys. Res. Commun. 178, 486-493, 1991

A/Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from t

A/Reference number: A44692; MUID:91315471

A/Accession: A44692

A/Molecule type: protein

A/Residues: 1-5 <OHT>

C/Keywords: amidated carboxyl end; D-amino acid; neuropeptide

F/2/Modified site: D-asparagine (Asn) #status experimental

F/5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 44.4%; Score 12; DB 2; Length 5;

Best Local Similarity 66.7%; Pred. No. 2e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 DFV 5

DB 1

RESULT 5

Leu-enkephalin - blue mussel

C/Species: Mytilus edulis (blue mussel)

C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000

C/Accession: B61445

R/Leung, M.K.; Stefano, G.B.

Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984

A/Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul

A/Reference number: B61445; MUID:84144823

A/Accession: B61445

A/Molecule type: protein

A/Residues: 1-5 <LEU>

C/Keywords: neuropeptide; opioid peptide

Query Match 44.4%; Score 12; DB 2; Length 5;

Best Local Similarity 50.0%; Pred. No. 2e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GDFV 5

DB 2 GGF 5

RESULT 6

Met-enkephalin - blue mussel

C/Species: Mytilus edulis (blue mussel)

C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000

C/Accession: A61445

R/Leung, M.K.; Stefano, G.B.

Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984

A/Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul

A/Reference number: A61445; MUID:84144823

A/Accession: A61445

A/Molecule type: protein

A/Residues: 1-5 <LEU>

C/Keywords: neuropeptide; opioid peptide

Query Match 44.4%; Score 12; DB 2; Length 5;

Best Local Similarity 50.0%; Pred. No. 2e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GDFV 5

DB 2 GGF 5

RESULT 7

T-cell receptor beta chain V-D-J region (100-44L) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C/Accession: P70513

R/Feeney, A.U.

J. Exp. Med. 174, 115-124, 1991

A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions

A/Reference number: P70509; MUID:91277601

A/Accession: P70513

A/Molecule type: not shown

A/Residues: 1-5 <FEF>

C/Keywords: adult thymus, strain BALB/c, clone 100-44L

Query Match 44.4%; Score 12; DB 2; Length 5;

Best Local Similarity 50.0%; Pred. No. 2e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GDFV 5

DB 2 GGF 5

RESULT 8

T-cell receptor beta chain V-D-J region (100-44L) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C/Accession: P70513

R/Feeney, A.U.

J. Exp. Med. 174, 115-124, 1991

A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions

A/Reference number: P70509; MUID:91277601

A/Accession: P70513

A/Molecule type: not shown

A/Residues: 1-5 <FEF>

C/Keywords: adult thymus, strain BALB/c, clone 100-44L

Query Match 44.4%; Score 12; DB 2; Length 5;

Best Local Similarity 50.0%; Pred. No. 2e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GDFV 5

DB 2 GGF 5

RESULT 9

T-cell receptor beta chain V-D-J region (100-44L) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C/Accession: P70513

R/Feeney, A.U.

J. Exp. Med. 174, 115-124, 1991

A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions

A/Reference number: P70509; MUID:91277601

A/Accession: P70513

A/Molecule type: not shown

A/Residues: 1-5 <FEF>

C/Keywords: adult thymus, strain BALB/c, clone 100-44L

Query Match 44.4%; Score 12; DB 2; Length 5;

Best Local Similarity 50.0%; Pred. No. 2e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GDFV 5

DB 2 GGF 5

RESULT 10

T-cell receptor beta chain V-D-J region (100-44L) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C/Accession: P70513

R/Feeney, A.U.

J. Exp. Med. 174, 115-124, 1991

A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions

A/Reference number: P70509; MUID:91277601

A/Accession: P70513

A/Molecule type: not shown

A/Residues: 1-5 <FEF>

C/Keywords: adult thymus, strain BALB/c, clone 100-44L

Query Match 44.4%; Score 12; DB 2; Length 5;

Best Local Similarity 50.0%; Pred. No. 2e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GDFV 5

DB 2 GGF 5



A:Residues: 1-5 <FE2>  
A:Experimental source: newborn thymus, strain BALB/c, clone 120-1S  
C:Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GD 3  
Db 3 GD 4

RESULT 8  
PT0538  
T-cell receptor beta chain V-D-J region (126-1F) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0538; PT0539; PT0603  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0538  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F  
A:Accession: PT0539  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE3>  
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1H  
A:Accession: PT0603  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: newborn thymus, strain BALB/c, clone 100-2AC  
C:Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GD 3  
Db 3 GD 4

RESULT 9  
PT0703  
T-cell receptor beta chain V-D-J region (135-1F) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0703  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0703  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GD 3  
Db 3 GD 4

RESULT 10  
PT0690  
T-cell receptor beta chain V-D-J region (140-1BD) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0690  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0690  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: day 18 fetal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GD 3  
Db 3 GD 4

RESULT 11  
PT0573  
T-cell receptor beta chain V-D-J region (141-1CC) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0573  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0573  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: day 18 fetal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GD 3  
Db 3 GD 4

RESULT 12  
PT0679  
T-cell receptor beta chain V-D-J region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0679; PT0708  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601  
A:Accession: PT0679  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-5 <FE2>

A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-23  
 A:Accession: P07078  
 A>Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-5 <FE2>  
 A:Experimental source: newborn thymus, strain BALB/c, 161-2B  
 C:Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GD 3  
 1 1  
 Db 3 GD 4

## RESULT 13

## ECXAA

antho-Ramide neuropeptide - sea anemone (Anthopleura elegantissima)  
 C:Species: Anthopleura elegantissima  
 C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 08-Dec-1995  
 C:Accession: A26666  
 R:Grimmelikhuizen, C.J.P.; Graff, D.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986  
 A:Title: Isolation of <Glu-Gly-Arg-Phe-NH2 (Antho-Ramide), a neuropeptide from sea anem  
 A:Reference number: A26666; MUID:87092339  
 A:Accession: A26666  
 A:Molecule type: protein  
 A:Residues: 1-4 <GRI>  
 C:Comment: The function of this peptide is not known but it could act as a transmitter a  
 C:Comment: Synthetic and natural peptides had identical properties.  
 C:Superfamily: Rfamamide neuropeptide  
 C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 40.7%; Score 11; DB 1; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 2e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RGDF 4  
 1 1  
 Db 1 QGRF 4

## RESULT 14

## A25844

antho-RF amide neuropeptide - sea pansy (Renilla koellikeri)  
 C:Species: Renilla koellikeri (Koelliker's sea pansy)  
 C:Date: 21-May-1988 #sequence\_revision 30-Sep-1993 #text\_change 11-Jul-1997  
 C:Accession: A25844  
 R:Grimmelikhuizen, C.J.P.; Groeger, A.  
 FEBS Lett. 211, 105-108, 1987  
 A:Title: Isolation of the neuropeptide pGlu-Gly-Arg-Phe-amide from the pennatulid Renilla  
 A:Reference number: A25844  
 A:Accession: A25844  
 A:Molecule type: protein  
 A:Residues: 1-4 <GRI>  
 C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 40.7%; Score 11; DB 2; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 2e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RGDF 4  
 1 1  
 Db 1 QGRF 4

## RESULT 15

## S39390

myosin-light-chain kinase (EC 2.7.1.117), smooth muscle - turkey (fragment)  
 C:Species: Meleagris gallopavo (common turkey)  
 C:Date: 19-Mar-1997 #sequence\_revision 10-Oct-1997 #text\_change 07-May-1999  
 C:Accession: S39390  
 R:Komatsu, H.; Ikebe, M.  
 Biochem. J. 296, 53-58, 1993  
 A:Title: Affinity labelling of smooth-muscle myosin light-chain kinase with 5'-[p-(f  
 A:Reference number: S39390; MUID:94071841  
 A:Accession: S39390  
 A:Molecule type: protein  
 A:Residues: 1-4 <KOM>  
 A:Experimental source: gizzard  
 C:Keywords: phosphotransferase; smooth muscle

Query Match 40.7%; Score 11; DB 2; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 2e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GDF 4  
 1 1  
 Db 2 GKF 4

Search completed: March 6, 2001, 09:47:29  
 Job time: 155 sec

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OM protein - protein search, using sw model

Run on: March 6, 2001, 09:48:22 ; Search time 12.72 Seconds

(without alignments)  
12.694 Million cell updates/sec

Title: US-09-081-522-7

Perfect score: 27

Sequence: 1 RSDPV 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues  
Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Swissprot\_39.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	44.4	5	UXA4_CHLTR	P38005 chlamydia t
2	37.0	5	TPIS_CANFA	P54714 canis famli
3	33.3	5	PAP2_PAPPA	P81864 pardachirus
4	29.6	5	TRM3_ECOLI	P13973 escherichia
5	25.9	4	FLRF_HIRME	P42561 hirudo medi
6	22.2	4	FMRF_MACNI	P01162 macrocallis
7	22.2	3	GRHM_HUMAN	P01157 homo sapien
8	22.2	3	LOXE_VIBRI	P24272 vibrio fisc
9	22.2	4	ACH1_ACHTU	P35904 achatina fu
10	22.2	4	DCML_PSECH	P19916 pseudomonas
11	22.2	4	BOS1_HUMAN	P02731 homo sapien
12	22.2	4	PAR3_HIRME	P42562 hirudo medi
13	22.2	4	FAK4_HIRME	P42563 hirudo medi
14	22.2	5	AL14_CARVA	P81817 carclaus ma
15	22.2	5	BIOA_CITFR	P13071 citrobacter
16	22.2	5	BIOA_SALTY	P16577 salmonella
17	22.2	5	SUGA_ACHRO	P18853 artipocsthi
18	22.2	5	UC22_MAIZE	P18991 acheta dcme
19	22.2	5	UF01_MOUSE	P38639 mus musculu
20	18.5	4	TUFT_HUMAN	P01858 homo sapien
21	18.5	5	PRCT_PERYM	P12678 periplaneta
22	14.8	4	RY01_YEAST	P36515 saccharomyc
23	7.4	4	DCMS_PSECH	P19918 pseudomonas
24	7.4	5	BP77_BOTIN	P30425 bothrops in
25	3.7	3	THYL_PIG	P01151 sus scrofa
26	3.7	5	BIOB_CITFR	P12997 citrobacter
27	1	1		
28	1	1		

## ALIGNMENTS

RESULT 1  
ID: UXA4\_CHLTR STANDARD; PRT: 5 AA.  
AC P38005;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).  
OS Chlamydia trachomatis.  
CC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
RN [1]  
RP SEQUENCE.  
RC STRAIN=L2/434/BJ;  
RA Binl L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,  
RA Comanducci M., Christensen G., Birkelund S., Vreton E., Ratti G.,  
RA Pallini V.;  
RL Submitted (SEP-1994) to the SWISS-PROT data bank.  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 4.5, ITS MW IS: 28 KDA.  
FT NON\_TER  
SQ SEQUENCE 5 AA: 474 MW: 75BA865AA800000 CRC64;

Query Match 44.4%; Score 12; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GD 3  
DB 3 GD 4

RESULT 2  
ID: TPIS\_CANFA STANDARD; PRT: 5 AA.  
AC P54714;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).  
GN TP11.  
OS Canis familiaris (Dog).  
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=HEART;  
RX MEDLINE=9816334; PubMed=9504812;  
RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
RT dog heart proteins";  
RL Electrophoresis 18:2795-2802(1997).  
CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE = DIHYDROXY-  
CC ACETONE PHOSPHATE.  
CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.  
DR HSC-2DPAGE; P54714; DOG.  
DR INTERPRO; IP8009652; -.  
DR PROSITE; PS00171; TIM; PARTIAL.  
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;  
FT NON\_TER  
SQ SEQUENCE 5 AA: 550 MW: 64444862C9A00000 CRC64;

Query Match 37.0%; Score 10; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 EV 5  
DB 11

```

Db      1 EV 2

RESULT 3
PAP2_PAPMA STANDARD: PRT: 5 AA.
ID      PAP2_PAPMA
AC      P81864;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      01-OCT-2000 (Rel. 40, Last annotation update)
DE      PARDAXIN II (FXII) (FRAGMENT).
OS      Pardachirus marmoratus (Red sea moose sole).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC      Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC      Soleioidae; Soleidae; Pardachirus.
RN      (1)
RP      SEQUENCE.
RC      TISSUE=SKIN SECRETION;
RX      MEDLINE=87057369; PubMed=3782138;
RA      Lazarovici P., Primor N., Loew L.M.;
RT      "Purification and pore-forming activity of two hydrophobic
RT      polypeptides from the secretion of the Red sea moose sole (Pardachirus
RT      marmoratus).";
RL      J. Biol. Chem. 261:16704-16713(1986).
CC      -1- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
CC      PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
CC      IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
CC      -1- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A Tetramer.
CC      -1- SUBCELLULAR LOCATION: SECRETED.
CM      Toxin.
KW      NON_TER
SQ      SEQUENCE 5 AA: 614 MW: 7769C9C8100000 CRC64;

Query Match
Best Local Similarity 33.3%; Score 9; DB 1; Length 5;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GDF 4
DB      1 GEF 3

RESULT 4
TRM3_ECOLI STANDARD: PRT: 5 AA.
ID      TRM3_ECOLI
AC      P13973;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-JAN-1990 (Rel. 13, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      TRAM PROTEIN (FRAGMENT).
GN      TRAM.
OS      Escherichia coli.
OC      Plasmid IncFII R100.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC      Escherichia.
RN      (1)
RP      SEQUENCE FROM N.A.
RX      MEDLINE=88227859; PubMed=2836369;
RA      Inamoto S., Yoshioaka Y., Ohtsuda E.;
RT      "Identification and characterization of the products from the tram
RT      and tram genes of plasmid R100.";
RL      J. Bacteriol. 170:2749-2757(1988).
CC      -1- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
CC      PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC      -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC      -1- SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC      the European Bioinformatics Institute. There are no restrictions on its

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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M20941; -; NOT_ANNOTATED_CDS.
DR      PIR; A32014; A32014.
KW      Conjugation; Plasmid; DNA-binding.
FT      NON_TER
SQ      SEQUENCE 5 AA: 634 MW: 661B1AA443500000 CRC64;

Query Match
Best Local Similarity 29.6%; Score 8; DB 1; Length 5;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RGD 3
DB      1 KND 3

RESULT 5
FLRF_HIRME STANDARD: PRT: 4 AA.
ID      FLRF_HIRME
AC      P42561;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      01-NOV-1995 (Rel. 32, Last annotation update)
DE      FLRFamide
OS      Hirudo medicinalis (Medicinal leech), and Hellsoma trivolvius (Snail).
OC      Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OC      Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
RN      (1)
RP      SEQUENCE.
RC      SPECIES=H.MEDICINALIS;
RX      MEDLINE=92195954; PubMed=1686933;
RA      Evans S.D., Fohl J., Kartsonis M.A., Calabrese R.L.;
RT      "Identification of Rfamde neuropeptides in the medicinal leech.";
RL      Peptides 12:697-908(1991).
RN      (2)
RP      SEQUENCE.
RC      SPECIES=H.TRIVOLVIVS; TISSUE=KIDNEY;
RX      MEDLINE=94286417; PubMed=7912428;
RA      Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT      "FMRFamide-related peptides from the kidney of the snail, Hellsoma
RT      trivolvius.";
RL      Peptides 15:31-36(1994).
CC      -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC      FAMILY.
CC      KW      Neuropeptide; Amidation.
CC      FT      MOD_RES 4
CC      SQ      SEQUENCE 4 AA: 582 MW: 69D40729A0000000 CRC64;

Query Match
Best Local Similarity 25.9%; Score 7; DB 1; Length 4;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 EV 5
DB      1 FL 2

RESULT 6
FMRF_MACNI STANDARD: PRT: 4 AA.
ID      FMRF_MACNI
AC      P01162;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      FMRFamide (PEAK C) (CARDIOEXCITATORY NEUROPEPTIDE).
OS      Macrocalliste nimbosa (Sun-ray clam), Nereis virens (Sandworm),
OS      Hirudo medicinalis (Medicinal leech), and Hellsoma trivolvius (Snail).

```

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;  
 OC Veneroidea; Veneridae; Macrocallista.  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC SPECIES-M.NIMBOSA; TISSUE-CEREBRAL PEDAL, AND VISCERAL CANGLION;  
 RX MEDLINE-77215956; PubMed-877582;  
 RA Price D.A., Greenberg M.J.;  
 RT "Structure of a molluscan cardioexcitatory neuropeptide."; Science 197;670-671(1977).  
 RN [2]  
 RP SEQUENCE, AND CHARACTERIZATION.  
 RC SPECIES-M.NIMBOSA; TISSUE-GANGLION;  
 RX MEDLINE-78012038; PubMed-909875;  
 RA Price D.A., Greenberg M.J.;  
 RT "Purification and characterization of a cardioexcitatory neuropeptide from the central ganglia of a bivalve mollusc."; Prep. Biochem. 7;261-281(1977).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES-N.VIRENS;  
 RX MEDLINE-90259866; PubMed-2342992;  
 RA Krajniak K.G., Price D.A.;  
 RT "Authentic FMRFamide is present in the polychaete Nereis virens."; Peptides 11;75-77(1990).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES-H.MEDICINALIS;  
 RX MEDLINE-92195954; PubMed-1686933;  
 RA Evans B.D., Pohl J., Karlsson M.A., Calabrese R.L.;  
 RT "Identification of Rfamde neuropeptides in the medicinal leech."; Peptides 12;897-908(1991).  
 RN [5]  
 RP SEQUENCE.  
 RC SPECIES-H.TRIVOLVIS; TISSUE-KIDNEY;  
 RX MEDLINE-94286417; PubMed-7912428;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma trivolvis."; Peptides 15;31-36(1994).  
 RN [6]  
 RP FUNCTION: MOAOCITIVE: CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF CARDING CONTRACTION.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.  
 CC PIR: A01426; ECKN.  
 DR PIR: A60418; A60418.  
 DR Neuropeptide; Amidation.  
 KW MOD\_RES 4 4 AMIDATION.  
 FT SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;  
 SQ

Query Match 25.9%; Score 7; DB 1; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 FV 5  
 1;  
 DB 1 FM 2

RESULT 7  
 GRWM\_HUMAN STANDARD; PRT: 3 AA.  
 ID GRWM\_HUMAN  
 NC P01157;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last annotation update)  
 DE GROWTH-MODULATING PEPTIDE.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE-77162369; PubMed-8583356;  
 RA Schlesinger D.H., Pickett L., Thaler M.M.;  
 RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine."; Experientia 33;324-325(1977).  
 CC -1- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.  
 DR PIR: A01421; GKHU.  
 SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 22.2%; Score 6; DB 1; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 G 2  
 1 G 1  
 DB 1 G 1

RESULT 8  
 LUXE\_VIBFI STANDARD; PRT: 3 AA.  
 ID LUXE\_VIBFI  
 AC P24272;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE LONG-CHAIN-FATTY-ACID-LUCIFERIN-COMPONENT LIGASE (EC 6.2.1.19) (ACYL-PROTEIN SYNTHETASE) (FRAGMENT).  
 GN LUXE.  
 OS Vibrio fischeri.  
 CC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91072225; PubMed-2254256;  
 RA Swartzman E., Kapoor S., Graham A.F., Weighen E.A.;  
 RT "A new Vibrio fischeri lux gene precedes a bidirectional termination site for the lux operon."; J. Bacteriol. 172;6797-6802(1990).  
 RN [2]  
 RP FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID. IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.  
 CC -1- CATALYTIC ACTIVITY: ATP + AN ACID + PROTEIN - AMP + PYROPHOSPHATE + AN ACYL-PROTEIN THIOLESTER.  
 CC -1- PATHWAY: SECOND STEP IN THE BIOLUMINESCENT FATTY ACID REDUCTASE COMPLEX.  
 CC -----  
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 CC -----  
 DR EMBL: M62812; -; NOT\_ANNOTATED\_CDS.  
 DR Luminescence; Ligase.  
 KW NON\_TER 1  
 FT SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;  
 SQ

Query Match 22.2%; Score 6; DB 1; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 D 3  
 1  
 DB 3 D 3

RESULT 9  
 ACHI\_ACHTU STANDARD; PRT: 4 AA.  
 ID ACHI\_ACHTU

AC P35904;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE ACHATTIN-1.  
 OS Achatina fulica (Giant African snail).  
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Stylomatophora;  
 CC Achatinacea; Achatinidae; Achatina.  
 RN [1]  
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.  
 RC STRAIN-FERUSSAC; TISSUE-GANGLION;  
 RA MEDLINE-8927351; PubMed-2597281;  
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,  
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Il P.,  
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;  
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina  
 RT fulica ferussac containing a D-amino acid residue."  
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).  
 RN [2]  
 RP CHARACTERIZATION.  
 RC STRAIN-FERUSSAC; TISSUE-HEART ATRIUM;  
 RA MEDLINE-91264856; PubMed-1675568;  
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;  
 RT "Purification of achatin-I from the atria of the African giant snail,  
 RT Achatina fulica, and its possible function."  
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RA MEDLINE-93014529; PubMed-1399265;  
 RA Iwashita T., in Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
 RA Iwashita T., Nomoto K.;  
 RT "Crystal structure and molecular conformation of achatin-I  
 RT D-amino acid residue."  
 RL Int. J. Pept. Protein Res. 39:258-264(1992).  
 CC -I- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY  
 CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY  
 CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE  
 CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.  
 DR PIR: A32480; A32480.  
 KM Hormone; D-amino acid.  
 FT MOD. RES. 2  
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DE CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (PC 1.2.99.2) (FRAGMENT).  
 OS Pseudomonas carboxydhydrogena.  
 CC Bacteria; Proteobacteria.  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE-9005678; PubMed-2818128;  
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;  
 RT "Homology and distribution of CO dehydrogenase structural genes in  
 RT carboxydtophic bacteria."  
 RL Arch. Microbiol. 152:335-341(1989).  
 CC -I- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR - CO(2) + REDUCED

CC ACCEPTOR.  
 CC -I- COFACTOR: MOLYBDENUM.  
 CC -I- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND  
 CC SMALL.  
 DR PIR: P10140; P10140.  
 KM Oxidoreductase; Molybdenum.  
 FT NOL. TER 4  
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F00000000 CRC64;  
 DT 01-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last annotation update)  
 DE EOSINOPHILROFACITIC PEPTIDES.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE-76078412; PubMed-1060093;  
 RA Goetzl E.J., Austen K.F.;  
 RT "Purification and synthesis of eosinophilrofacit tetrapeptides of  
 RT human lung tissue: identification as eosinophil chemotactic factor of  
 RT anaphylaxis."  
 RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).  
 CC -I- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG  
 CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS  
 CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING  
 CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE  
 CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.  
 DR PIR: A03190; ETHUL.  
 FT VARIANT 1  
 SQ SEQUENCE 4 AA; 390 MW; 6E05B862A00000000 CRC64;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFAMIDE-LIKE NEUROPEPTIDE YLR-AMIDE.  
 OS Hirudo medicinalis (Medicinal leech).  
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;  
 CC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE-92195954; PubMed-1686933;  
 RA Evans B.D., Pohl J., Karlsonis M.A., Calabrese R.L.;

RT "Identification of Rfamidae neuropeptides in the medicinal leech."  
 RL Peptides 12:897-908(1991).  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC Neuropeptide; Amidation.  
 FT MOD\_RES 4  
 SO SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 22.2%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 F 4  
 DB 4 F 4

RESULT 13  
 FARA\_HIRME STANDARD; PRT; 4 AA.  
 ID FARA\_HIRME  
 AC P42563;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFAMIDE-LIKE NEUROPEPTIDE YMRF-AMIDE.  
 OS Hirudo medicinalis (Medicinal leech).  
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;  
 CC Arynchobellida; Hirudiniiformes; Hirudiniidae; Hirudo.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE-92195954; PubMed-1686933;  
 RA Evans B.D., Pohl J., Kartsotis M.A., Calabrese R.L.;  
 RT "Identification of Rfamidae neuropeptides in the medicinal leech."  
 RL Peptides 12:897-908(1991).  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC Neuropeptide; Amidation.  
 FT MOD\_RES 4  
 SO SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 22.2%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 F 4  
 DB 4 F 4

RESULT 14  
 AL14\_CARMA STANDARD; FRT; 5 AA.  
 ID AL14\_CARMA  
 AC P81817;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CARCINOSTATIN 14.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;  
 RX MEDLINE-98121193; PubMed-9461295;  
 RA Duye H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas."  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.

CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC Neuropeptide; Amidation; Multi-gene family.  
 FT MOD\_RES 5  
 SO SEQUENCE 5 AA; 586 MW; 672879D5AB30000000 CRC64;

Query Match 22.2%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 F 4  
 DB 3 F 3

RESULT 15  
 BIOA\_CITFR STANDARD; PRT; 5 AA.  
 ID BIOA\_CITFR  
 AC P13071;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DE ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE  
 DE (EC 2.6.1.52) (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA  
 DE AMINOTRANSFERASE) (FRAGMENT).  
 GN BIOA.  
 OS Citrobacter freundii.  
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 CC Citrobacter.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-8906280; PubMed-2971595;  
 RA Shuan D., Campbell A.;  
 RT "Transcriptional regulation and gene arrangement of Escherichia coli,  
 RT Citrobacter freundii and Salmonella typhimurium biotin operons."  
 RL Gene 67:203-211(1988).  
 CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-  
 CC OXONONANOATE -> S-ADENOSYL-4-METHYLTHIO-2-OXOBUTANOATE +  
 CC 7,8-DIAMINONONANOATE.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- PATHWAY: BIOTIN BIOSYNTHESIS.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.

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 CC -----

DR EMBL; M21922; CAB25179.1; -  
 DR INTERPRO; IPR000954; -  
 DR PROSITE; PS00600; AA TRANSFER CLASS 3; PARTIAL.  
 KW Biotin biosynthesis; transferase; aminotransferase;  
 KW Pyridoxal phosphate.  
 FT NON\_TER 5  
 SO SEQUENCE 5 AA; 582 MW; 6AAAB1BA6F000000 CRC64;

Query Match 22.2%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 D 3  
 DB 4 D 4

Search completed: March 6, 2001, 09:48:22

Job time: 180 sec

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OM protein - protein search, using sw model

Run on: March 6, 2001, 09:48:05 ; Search time 32.72 Seconds  
(without alignments)  
17.911 Million cell updates/sec

Title: US-09-081-522-7  
Perfect score: 27  
Sequence: 1 RGDV 5

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 374700 seqs, 117207915 residues  
Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	44.4	5	13	P82070
2	10	37.0	5	13	P82099
3	9	33.3	5	13	P82073
4	9	33.3	5	13	P82100
5	8	29.6	5	13	P82071
6	8	29.6	5	13	P82072
7	4	14.8	4	11	Q08433
8	2	7.4	5	10	Q99007

## ALIGNMENTS

RESULT 1  
ID P82070 PRELIMINARY: PRT: 5 AA.  
AC P82070: (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE RUBELIDIN 1.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
OC Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE-SKIN SECRETION:  
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
RA Tyler M.O., Wallace J.C.;  
RT "The structure of new peptides from the Australian red tree frog  
'Litoria rubella', the skin peptide profile as a probe for the study  
of evolutionary trends of amphibians."  
RL Aust. J. Chem. 49:955-963(1996)  
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
CC ANTIBIOTIC ACTIVITY.  
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
CC -1- MASS SPECTROMETRY: MW=598; METHOD=FAE.  
KW Amphibian skin.  
SQ SEQUENCE 5 AA: 598 MW: 6DD9C9CAB2A00000 CRC64;

Query Match 44.4%; Score 12; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2  
ID P82099 PRELIMINARY: PRT: 5 AA.  
AC P82099:  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE ELECTRIN 3.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
OC Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE-SKIN SECRETION:  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
Litoria electrica. Comparison with the skin peptides from Litoria  
rubella."  
RL Aust. J. Chem. 52:0-0(1999).  
KW Amphibian skin; Amidation.  
FT MOD RES 5  
SQ SEQUENCE 5 AA: 630 MW: 658761F2C9A00000 CRC64;

Query Match 37.0%; Score 10; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3  
ID P82073 PRELIMINARY: PRT: 5 AA.  
AC P82073:  
DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE RUBELLIDIN 3.2.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 CC Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-SKIN SECRETION;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 'Litoria rubella', the skin peptide profile as a probe for the study  
 of evolutionary trends of amphibians.";  
 RT Litoria rubella.  
 RL Aust. J. Chem. 52:0-0(1999).  
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
 ANTI-BIOTIC ACTIVITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 CC Amphibian skin.  
 KW Amphibian skin.  
 SO SEQUENCE 5 AA; 570 MW; 71A9C9C82A00000 CRC64;

Query Match 33.3%; Score 9; DB 13; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 3.7e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GDF 4  
 DB 2 GFF 4

RESULT 4  
 ID P82100 PRELIMINARY; PRT: 5 AA.  
 AC P82100;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE ELECTRIN 4.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 CC Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-SKIN SECRETION;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 'Litoria rubella', the skin peptide profile as a probe for the study  
 of evolutionary trends of amphibians.";  
 RT Litoria rubella.  
 RL Aust. J. Chem. 52:0-0(1999).  
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
 ANTI-BIOTIC ACTIVITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 CC Amphibian skin; Amidation.  
 FT MOD\_RES 5  
 SO SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 33.3%; Score 9; DB 13; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 3.7e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 EV 5  
 DB 1 FI 2

RESULT 5  
 ID P82071 PRELIMINARY; PRT: 5 AA.  
 AC P82071;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE RUBELLIDIN 2.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 CC Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE-SKIN SECRETION;  
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 'Litoria rubella', the skin peptide profile as a probe for the study  
 of evolutionary trends of amphibians.";  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
 ANTI-BIOTIC ACTIVITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 CC -1- MASS SPECTROMETRY: MM=626; METHOD=FAE.  
 CC Amphibian skin.  
 KW Amphibian skin.  
 SO SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 29.6%; Score 8; DB 13; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 3.7e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 DF 4  
 DB 2 EF 3

RESULT 6  
 ID P82072 PRELIMINARY; PRT: 5 AA.  
 AC P82072;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE RUBELLIDIN 3.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 CC Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE-SKIN SECRETION;  
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 'Litoria rubella', the skin peptide profile as a probe for the study  
 of evolutionary trends of amphibians.";  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
 ANTI-BIOTIC ACTIVITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 CC -1- MASS SPECTROMETRY: MM=655; METHOD=FAE.  
 CC Amphibian skin; Amidation.  
 FT MOD\_RES 5  
 SO SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 29.6%; Score 8; DB 13; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 3.7e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 DF 4  
 DB 2 EF 3

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RESULT 7
008433 PRELIMINARY; PRT; 4 AA.
AC 008433:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMblrel. 09, Last annotation update)
DE UDP-GLUCURONOSYLTTRANSFERASE, MICROSMAL (EC 2.4.1.17) (UDPGR)
DE (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUNN;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROsome.
DR EMBL, S38636; AB019259.1;
FT Transferase; Glycosyltransferase; Microsome; Multigene family.
FT NON_TER 1
FT NON_TER 4
FT NON_TER 4
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

```

```

Query Match 14.8%; Score 4; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 5 V 5
DB 2 V 2

```

```

RESULT 8
099007 PRELIMINARY; PRT; 5 AA.
AC 099007:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).
GN AMY1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V., Close T.J.;
RT "Control of transient expression of chimeric genes by gibberellic
RT acid and abscisic acid in protoplasts prepared from mature barley
RT aleurone layers.";
RL Plant Mol. Biol. 16:713-721(1991).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC BARLEY.
DR EMBL, X54643; CAA38455.1;
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family.

```

```

FT NON_TER 5
SQ SEQUENCE 5 AA; 600 MW; 61E344DD6F00000 CRC64;

```

```

Query Match 7.4%; Score 2; DB 10; Length 5;
Best Local Similarity 0.0%; Pred. No. 3.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 R 1
DB 4 K 4

```

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Search completed: March 6, 2001, 09:48:05
Job time: 191 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:45:58 ; Search time 14.72 Seconds  
(without alignments)  
34.844 Million cell updates/sec

Title: US-09-081-522-8  
Perfect score: 83  
Sequence: 1 YTRAACKPYTR32VF 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 107883

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A.Geneseq\_36:\*

- 1: /SIDSL/gcgdata/geneseq/geneseqp/AA1980.DAT:\*
- 2: /SIDSL/gcgdata/geneseq/geneseqp/AA1981.DAT:\*
- 3: /SIDSL/gcgdata/geneseq/geneseqp/AA1982.DAT:\*
- 4: /SIDSL/gcgdata/geneseq/geneseqp/AA1983.DAT:\*
- 5: /SIDSL/gcgdata/geneseq/geneseqp/AA1984.DAT:\*
- 6: /SIDSL/gcgdata/geneseq/geneseqp/AA1985.DAT:\*
- 7: /SIDSL/gcgdata/geneseq/geneseqp/AA1986.DAT:\*
- 8: /SIDSL/gcgdata/geneseq/geneseqp/AA1987.DAT:\*
- 9: /SIDSL/gcgdata/geneseq/geneseqp/AA1988.DAT:\*
- 10: /SIDSL/gcgdata/geneseq/geneseqp/AA1989.DAT:\*
- 11: /SIDSL/gcgdata/geneseq/geneseqp/AA1990.DAT:\*
- 12: /SIDSL/gcgdata/geneseq/geneseqp/AA1991.DAT:\*
- 13: /SIDSL/gcgdata/geneseq/geneseqp/AA1992.DAT:\*
- 14: /SIDSL/gcgdata/geneseq/geneseqp/AA1993.DAT:\*
- 15: /SIDSL/gcgdata/geneseq/geneseqp/AA1994.DAT:\*
- 16: /SIDSL/gcgdata/geneseq/geneseqp/AA1995.DAT:\*
- 17: /SIDSL/gcgdata/geneseq/geneseqp/AA1996.DAT:\*
- 18: /SIDSL/gcgdata/geneseq/geneseqp/AA1997.DAT:\*
- 19: /SIDSL/gcgdata/geneseq/geneseqp/AA1998.DAT:\*
- 20: /SIDSL/gcgdata/geneseq/geneseqp/AA1999.DAT:\*
- 21: /SIDSL/gcgdata/geneseq/geneseqp/AA2000.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	15	16	R82390
2	83	100.0	15	18	W33058
3	83	100.0	15	19	W41102
4	83	100.0	15	19	W41244
5	48	57.8	15	16	R67663
6	36	43.4	9	19	W66820
7	36	43.4	9	20	W97014
8	30	36.1	10	19	W68121
9	30	36.1	10	19	W68122
10	30	36.1	10	19	W68119
11	29	34.9	11	13	R24067
12	28	33.7	11	11	R06020

13	28	33.7	12	16	R76241	Human Fas peptide
14	28	33.7	12	21	Y84806	Internal peptide o
15	28	33.7	13	17	R95859	Heterologous prote
16	27.5	33.1	11	21	Y81884	Yeast SMI protein
17	27	32.5	8	15	R50462	Antiproliferative
18	27	32.5	10	18	W22349	Human bone apposit
19	27	32.5	10	19	W68120	Human bone apposit
20	27	32.5	10	19	W68123	Human bone apposit
21	27	32.5	10	19	W68129	Human bone apposit
22	27	32.5	10	19	W68130	Human bone apposit
23	27	32.5	10	19	W68109	Human bone apposit
24	27	32.5	10	19	W68117	Human bone apposit
25	27	32.5	10	19	W68124	Human bone apposit
26	27	32.5	10	19	W68125	Human bone apposit
27	27	32.5	10	19	W68128	Human bone apposit
28	27	32.5	11	18	W22356	Human bone apposit
29	27	32.5	11	18	W58116	Human bone apposit
30	27	32.5	14	18	W22348	Human bone apposit
31	27	32.5	14	19	W68108	Human bone apposit
32	27	32.5	15	18	W22347	Human bone apposit
33	27	32.5	15	19	W68107	Human bone apposit
34	26	31.3	9	13	R21425	Matrix peptide fro
35	26	31.3	9	20	W97047	Peptide used to in
36	26	31.3	10	19	W54456	Human native angio
37	26	31.3	10	19	W96982	Human native angio
38	26	31.3	10	21	Y70262	Peptide encoded by
39	26	31.3	12	18	W23803	VEGF/VPF antigen s
40	26	31.3	12	19	W74628	Amino acid sequenc
41	26	31.3	12	19	W74689	Amino acid sequenc
42	26	31.3	12	19	W74690	Amino acid sequenc
43	26	31.3	12	19	W55952	Human vascular per
44	26	31.3	12	19	W55953	Human vascular per
45	26	31.3	12	19	W55951	Human vascular per

#### ALIGNMENTS

RESULT 1	
R82390	R82390 standard: peptide; 15 AA.
XX	
AC	R82390;
DT	03-MAR-1996 (first entry)
XX	
DE	Integrin alpha-v-beta-3 inhibitor peptide no. 62880.
XX	
KW	Integrin: alpha-v-beta-3; inhibitor: angiogenesis; antagonist;
XX	fibrinogen; inflammation; apoptosis; restenosis.
OS	Synthetic.
XX	
PN	W09525543-A1.
XX	
PD	28-SEP-1995.
XX	
PF	09-MAR-1995; 95WO-US03035.
XX	
PR	30-DEC-1994; 34US-036665.
XX	
PR	18-MAR-1994; 94US-0210715.
XX	
PA	(SCRI ) SCRI PPS RES INST.
XX	
PI	Brooks F, Cheshash DA;
XX	
DR	WPI; 1995-34463/44.
XX	
PT	Inhibition of angiogenesis in a tissue, e.g. following angioplasty
PT	- by admin. of a compsn. comprising an alpha-v-beta3 antagonist;
PT	useful for regression of established tumours, treating inflamed
PT	tissue, etc.
XX	



CC organic mimetic compound. They can be used to inhibit angiogenesis  
 CC in inflamed tissue (for treatment of arthritis or rheumatoid  
 CC arthritis), in solid tumours or metastases (particularly to induce  
 CC regression or inhibit tumour growth), and in ocular disorders such  
 CC as diabetic retinopathy and macular degeneration, as well as to  
 CC treat stenosis (all claimed).

XX Sequence 15 AA;

Query Match 100.0%; Score 83; DB 19; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.5e-08;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTAACKPQVTRGDVF 15

Db 1 ytaackpqrtrgdvf 15

RESULT 4

W41244

W41244 standard; protein; 15 AA.

09-JUN-1998 (first entry)

Alpha-v-beta-5 antagonistic peptide 62880.

Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;

angiogenesis; tumour growth; stenosis; neovascularisation.

Synthetic.

Key Location/Qualifiers

Misc-difference 1..15 /note= "peptide is made cyclic via the first and last residues"

W09745447-A1.

04-DEC-1997.

30-MAY-1997; 97MO-US09099.

31-MAY-1996; 96US-0018733.

31-MAY-1996; 96US-0013869.

(SCRI ) SCRIIPS RES INST.

Brooks P, Cheres DA, Friedlander M;

WPI; 1998-041758/04.

Packaging material containing polypeptide antagonist of alphav,

beta5 integrin - used for inhibition of angiogenesis, and for

treating tumours, inflammation, eye diseases etc.

Disclosure; Page 41; 117pp; English.

The present peptide represents an alpha-v-beta-5 integrin antagonists.

Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5

can inhibit angiogenesis. The specification describes a novel

labelled package that contains an inhibitor of angiogenesis i.e. an

alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.

The antagonists are used to inhibit angiogenesis in inflamed tissues, in

solid tumours or metastases, and in a wide range of ocular disorders

(e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or

CC The antagonists particularly inhibit neovascularisation where this is  
 CC induced by cytokines, e.g. transforming growth factor alpha, epidermal  
 CC growth factor or especially vascular endothelial growth factor.  
 CC note: this sequence does not appear in the specification; it was created  
 CC using information provided.

XX Sequence 15 AA;

Query Match 100.0%; Score 83; DB 19; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.5e-08;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTAACKPQVTRGDVF 15

Db 1 ytaackpqrtrgdvf 15

RESULT 5

R67663

R67663 standard; peptide; 15 AA.

07-AUG-1995 (first entry)

Synthetic peptide of cell-adhesive molecule vitronectin.

Influenza; nucleoprotein; immunoglobulin; NP; CCR; Ig;

complementarity determining region; epitope; antigen; tolerance;

hypersensitivity; immunity; pathogen.

Synthetic.

W09428026-A.

08-DEC-1994.

25-MAY-1994; 94MO-US06090.

28-MAY-1993; 93US-0068895.

(REGC ) UNIV CALIFORNIA.

Billette R, Zanetti M;

WPI; 1995-022720/03.

New immunoglobulin contg. influenza virus nucleoprotein epitope

- useful in vaccines to induce specific anti-viral immunity, also

related DNA, vectors and transfected host cells

Example 1B; Page 23; 62pp; English.

Influenza virus nucleoprotein (NP) epitopes may be inserted into

immunoglobulin complementarity determining regions to render the

immunoglobulin molecule antigenic, making it useful as a vaccine.

Such antigenised antibodies can be used to induce

tolerance to particular antigens (including those associated with

autoimmune diseases); to down-regulate hypersensitivity to allergens,

or to provide active or passive immunity against pathogenic antigens.

The antigenic immunoglobulins are fully functional as regards

localisation on cell or receptor sites and elicit cytotoxic T

lymphocytes specific for the incorporated epitope. This synthetic

XX Sequence 15 AA;

Query Match 57.8%; Score 48; DB 15; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.053;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTAACKPQVTRGDVF 15

Db 1 ytaackpqrtrgdvf 15

QY 7 POYTRGDVDF 15  
 DB 2 PYVTRGDVDF 10

## RESULT 6

W66820  
 ID W66820 standard; peptide; 9 AA.

AC W66820;

DT 10-DEC-1998 (first entry)

XX Peptide used in purification of vitronectin receptor.

XX bone resorption; pharmacore; angiogenesis; restenosis; integrin receptor;

KW alpha v beta 3 integrin receptor; osteoclast; vitronectin receptor;

XX affinity chromatography.

OS Synthetic.

PN US5807819-A.

PD 15-SEP-1998.

PF 12-APR-1995; 94US-0421698.

PR 12-APR-1995; 95US-0421698.

PR 15-APR-1994; 94US-0227316.

PR 08-SEP-1994; 94US-0303052.

XX (LJOL-) LA JOLLA CANCER RES CENT.

PI Cheng S, Ingram R, Mullen D, Tschopp JF;

DR WPI; 1998-555601/47.

XX Use of peptide derivatives which can alter integrin receptor binding

PT - for altering bone resorption, treating angiogenesis or restenosis

PT and altering integrin receptor mediated interactions

XX Example 2; Column 22; 87pp; English.

XX The invention relates to peptides that are useful for inhibiting bone

CC resorption, angiogenesis or restenosis, and for altering integrin

CC receptor-mediated interactions, especially alpha v beta 3 integrin

CC receptor-mediated binding of cells to a matrix. They may be used for

CC reducing or inhibiting osteoclast binding to a matrix. Administration is

CC oral, parenteral, topical, transdermal or by inhalation. The present

CC sequence represents a peptide used in an affinity chromatography column for

CC purification of the human alpha v beta 3 vitronectin receptor.

XX Sequence 9 AA;

SO Query Match 43.4%; Score 36; DB 19; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.1e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VTRGDVDF 15  
 DB 1 VTRGDVDF 7

RESULT 7  
 ID W97014 standard; peptide; 9 AA.

XX W97014;  
 XX 26-APR-1999 (first entry)

DE Peptide used to inhibit bone resorption, angiogenesis and restenosis.  
 XX RGD-peptide; bone resorption; angiogenesis; restenosis;  
 KW integrin receptor mediated interaction; binding; osteoclast; bone.

XX Synthetic.

OS US5849865-A.

PN 15-DEC-1998.

PD 12-APR-1995; 95US-0421695.

PR 12-APR-1995; 95US-0421695.

PR 13-APR-1994; 94US-0227316.

PR 08-SEP-1994; 94US-0303052.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

PI Cheng S, Ingram R, Mullen D, Tschopp JF;

DR WPI; 1999-179486/15.

XX RGD peptides - that modulate integrin-mediated cell-matrix binding

PS Disclosure; Columns 35-36; 90pp; English.

XX The present peptide represents a non-naturally occurring

CC Arg-lyl-Asp (RGD)-containing peptide. The peptide may be

CC useful for reducing or inhibiting bone resorption, angiogenesis

CC or restenosis, and for altering an integrin receptor mediated

CC interaction. The peptide may also be used to inhibit the binding

CC of an osteoclast to bone.

XX Sequence 9 AA;

SO Query Match 43.4%; Score 36; DB 20; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.1e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VTRGDVDF 15  
 DB 1 VTRGDVDF 7

RESULT 8  
 ID W68121 standard; peptide; 10 AA.

XX W68121;  
 AC 30-SEP-1998 (first entry)

XX Human bone apposition peptide modified active fragment 11.

DE Bone stimulatory activity; BSA; bone growth; bone reduction disease;

KW osteoporosis; bone apposition.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 8 /label= D8E

FT /note="wild-type (W68109) Asp is replaced by Glu"

XX W09826070-A1.

XX 18-JUN-1998.

XX 11-DEC-1997; 97WO-CA00967.



PR 11-DEC-1996; 96US-0763458.  
XX  
PA (GENS-) GENSCI REGENERATION SCI INC.  
XX  
PI Tam CS:  
XX  
DR WPI: 1998-348527/30.  
DR N-PSDB; V41207.  
XX  
PT New bone growth stimulating factors - used to develop products for  
PT the diagnosis, prevention and treatment of bone reduction disease,  
PT particularly osteoporosis  
PS  
PS Claim 35; Page 56; 82pp; English.  
XX  
CC This is a modified active fragment of the human bone apposition peptide  
CC (W68101). Peptides derived from this sequence (W68101) can exhibit bone  
CC stimulatory activity (BSA). The specification provides active peptide  
CC sequences as shown in W68103 to W68109, W68117 to W68123 and W68129 to  
CC W68133 which promote bone growth in mammals. These peptides have in vivo  
CC BSA in mammals and increase the mineral content in bones. A vector  
CC comprising a DNA sequence encoding the BSA activity exhibiting peptides  
CC or their analogues can be used to recombinantly produce the polypeptides.  
CC The polypeptides can be used for the stimulation of bone growth. They can  
CC be used in the prevention and treatment of a bone reduction disease,  
CC particularly osteoporosis. The products can also be used for detection  
CC and diagnosis.  
XX  
SQ Sequence 10 AA:  
  
Query Match 36.1%; Score 30; DB 19; Length 10;  
Best Local Similarity 83.3%; Pred. No. 41;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YTAECK 6  
Db :|||||  
5 htaeck 10  
  
RESULT 9  
W68122  
ID W68122 standard; peptide; 10 AA.  
XX  
AC W68122;  
XX  
DT 30-SEP-1998 (first entry)  
XX  
DE Human bone apposition peptide modified active fragment 12.  
XX  
KW Bone stimulatory activity; BSA; bone growth; bone reduction disease;  
KW osteoporosis; bone apposition.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH MISC-difference 3 /label= N3Q  
FT /note= "wild-type (W68109) Asn is replaced by Gln"  
FT MISC-difference 8 /label= DBE  
FT /note= "wild-type (W68109) Asp is replaced by Glu"  
XX  
FN W09826070-A1.  
XX  
PD 18-JUN-1998.  
XX  
PE 11-DEC-1997; 97WO-CA00967.  
XX  
PR 11-DEC-1996; 96US-0763458.  
XX  
PA (GENS-) GENSCI REGENERATION SCI INC.

XX  
PI Tam CS:  
XX  
DR WPI: 1998-348527/30.  
DR N-PSDB; V41208.  
XX  
PT New bone growth stimulating factors - used to develop products for  
PT the diagnosis, prevention and treatment of bone reduction disease,  
PT particularly osteoporosis  
PS  
PS Claim 35; Page 57; 82pp; English.  
XX  
CC This is a modified active fragment of the human bone apposition peptide  
CC (W68101). Peptides derived from this sequence (W68101) can exhibit bone  
CC stimulatory activity (BSA). The specification provides active peptide  
CC sequences as shown in W68103 to W68109, W68117 to W68123 and W68129 to  
CC W68133 which promote bone growth in mammals. These peptides have in vivo  
CC BSA in mammals and increase the mineral content in bones. A vector  
CC comprising a DNA sequence encoding the BSA activity exhibiting peptides  
CC or their analogues can be used to recombinantly produce the polypeptides.  
CC The polypeptides can be used for the stimulation of bone growth. They can  
CC be used in the prevention and treatment of a bone reduction disease,  
CC particularly osteoporosis. The products can also be used for detection  
CC and diagnosis.  
XX  
SQ Sequence 10 AA:  
  
Query Match 36.1%; Score 30; DB 19; Length 10;  
Best Local Similarity 83.3%; Pred. No. 41;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YTAECK 6  
Db :|||||  
5 htaeck 10  
  
RESULT 10  
W68119  
ID W68119 standard; peptide; 10 AA.  
XX  
AC W68119;  
XX  
DT 30-SEP-1998 (first entry)  
XX  
DE Human bone apposition peptide modified active fragment 9.  
XX  
KW Bone stimulatory activity; BSA; bone growth; bone reduction disease;  
KW osteoporosis; bone apposition.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH Modified-site 1 /note= "N-terminal acetylation"  
FT MISC-difference 3 /label= N3Q  
FT /note= "wild-type (W68109) Asn is replaced by Gln"  
FT MISC-difference 8 /label= DBE  
FT /note= "wild-type (W68109) Asp is replaced by Glu"  
FT Modified-site 10 /note= "C-terminal amide"  
XX  
FN W09826070-A1.  
XX  
PD 18-JUN-1998.  
XX  
PE 11-DEC-1997; 97WO-CA00967.  
XX  
PR 11-DEC-1996; 96US-0763458.  
XX

PA	(GENS-)	GENSCI REGENERATION SCI INC.
XX		
XX		
PI	Tam CS:	
XX		
DR	WPI: 1998-346527/30.	
XX		
PT	New bone growth stimulating factors - used to develop products for	
PT	the diagnosis, prevention and treatment of bone reduction disease,	
PT	particularly osteoporosis	
PS	Claim 14; Page 32; 82pp; English.	
XX		
CC	This is a modified active fragment of the human bone apposition peptide	
CC	(W68101). Peptides derived from this sequence (W68101) can exhibit bone	
CC	stimulatory activity (BSA). The specification provides active peptide	
CC	sequences as shown in W68103 to W68109, W68117 to W68123 and W68129 to	
CC	W68133 which promote bone growth in mammals. These peptides have <i>in vivo</i>	
CC	BSA in mammals and increase the mineral content in bones. A vector	
CC	comprising a DNA sequence encoding the BSA activity exhibiting peptides	
CC	or their analogues can be used to recombinantly produce the polypeptides.	
CC	The polypeptides can be used for the stimulation of bone growth. They can	
CC	be used in the prevention and treatment of a bone reduction disease, and	
CC	particularly osteoporosis. The products can also be used for detection	
XX	and diagnosis.	
XX		
SO	Sequence 10 AA:	

Query Match	36.1%	Score :0	DB	19	Length	10			
Best Local Similarity	83.3%	Pred. No.	41						
Matches	5	Conservative	1	Mismatches	0	Indels	0	Gaps	0
QY	1	YTAACK	6						
		:							
Db	5	hlaeck	10						

```

RESULT  11
R24067
ID      R24067  standard; Protein; 11 AA.

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DT 27-NOV-1992 (first entry)

DE Cell-to-cell binding inhibiting peptide subunit (6).  
DE

**KW** Adhesion; integrin; multimer.

Synthetic.

AA	FH	Key	Location/Qualifiers

Cross-links	2,2,7,7-tetrachloro-4-methyl-5-norbornene-2,3-dicarboxylic anhydride	2,2,7,7-tetrachloro-4-methyl-5-norbornene-2,3-dicarboxylic anhydride
FT	multimers of sequence linked by interchain disulfide bonds with Cys residues	multimers of sequence linked by interchain disulfide bonds with Cys residues
FT		

AA  
PN W09208476-A.

PD 29-MAY-1992.

AA 07-NOV-1991; 91WO-US08328.  
PF

07-NOV-1990; 90US-0610363.

PA (Scripps Res Inst.

PI Houghten RA, Ruggeri ZM;

WPI; 1992-199940/24.

Peptides inhibiting

PT diseases associated with platelet aggregation

XX Claim 67; Page 69; 70pp; English.  
PS  
XX  
XX A peptide which inhibits binding of adhesion moles. to cells  
CC expressing interins may comprise two subunits having the sequence  
CC below, held together by an interchain stable bond. The sequence  
CC RCD is in each of the subunits.  
XX  
XX Sequence 11 Ab;  
SQ

Query Match	34.9%	Score 29	DB 13	Length 11
Best Local Similarity	50.0%	Pred. No. 68		
Matches	5	Conservative	3	Mismatches
			2	Indels
			0	Gaps
				0

QY	5	CKPQVTBGDV	14
	1	:	:
	:	:	:
	:	:	:
	:	:	:
Db	2	crrrrsrçdv	11

RESULT	12	:
R06020		
ID	R06020	standard; protein; 11 AA.
vv		

DT 20-NOV-1990 (first entry)

DE Oligopeptide, antigenic to N.meningitidis.

KW . Meningococcal disease; meningitis; vaccine;  
vaccination  
vaccine . Outer membrane protein; de-

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W09006595-A

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PD 28-JUN-1990

XX 19-DEC-1980. 89WO-11505678  
DE

XX	26--TTN-1989.	89NT.-0001612
DB		

PR	19-DEC-1988;	88NL-0003111.
PR	05-JAN-1989;	89NL-0000030.

PR 05-JAN-1989; 89NL-0000036.  
XX

PA (PRAX-) PRAXIS BIOLOGICS IN.  
PA (VOJK-) BIKINSINST VOJKSGEZONDH.

XX SEID R., PARADISO P., POOLMAN J.T., HOOGERHOFF P., WIERTZ F.T.;  
PT

PI VANDERLEY P, HECKELS JE, CLARKE IN;  
XX

DR WPT; 1990-224326/29.  
XX

PT Meningococcus class 1 outer-membrane protein vaccine - useful to immunise against meningococcal disease.

XX  
PS  
Claim 50: Page 102: 120pp: English.

XX Peptides derived from outer membrane, encoding homo/heterologous CC

product such as a antigen-flagelin fusion protein, are useful in eliciting a strong and wide ranging immune response against most

CC serotypes.  
XX

SQ	Sequence	11 AA
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Query Match	33.7%	Score 28	DB 11	Length 11
Similarity	71.4%	Pred. Nc.	1e+02	
Best Local				
5, Conservative	1	Mismatches	1	Indels 0
				Gaps 0

QY 6 KPOVTRG 12  
:|||||

Db 1 qpvvng 7

RESULT 13

ID R76241 standard; peptide; 12 AA.

XX R76241;

AC R76241;

XX 06-NOV-1995 (first entry)

DE Human Fas peptide 147-152/174-179.

XX Fas-delta-TM; transmembrane deletion; apoptosis; antibody;

KW adoptive immunotherapy; transgenic animal.

XX Synthetic.

OS Synthetic.

XX W09513701-A.

PN W09513701-A.

XX 26-MAY-1995.

PD 26-MAY-1995.

XX 15-NOV-1994; 94MO-US13173.

PE 15-NOV-1994; 94MO-US13173.

XX 15-NOV-1993; 93US-0152443.

PR 15-NOV-1993; 93US-0152443.

XX (LXRB-) LXR BIOTECHNOLOGY INC.

PA (LXRB-) LXR BIOTECHNOLOGY INC.

XX Barr PJ, Klefer MC, Shapiro JP;

PI Barr PJ, Klefer MC, Shapiro JP;

XX WPI: 1995-200120/26.

DR WPI: 1995-200120/26.

XX New nucleic acid encoding Fas protein without its trans-membrane region

PT - and related vectors, transformed cells, transgenic animals, protein and

PT antibodies, useful for control of Fas mediated apoptosis

XX Disclosure: Fig.4; 38pp; English.

PS Synthetic peptides corresp. to the extracellular, transmembrane

CC (TM) and truncated TM regions of fas proteins, given in R75239-41,

CC respectively, were used to raise antibodies useful in detecting

CC biologically important fas molecules.

CC Sequence 12 AA:

SO

Query Match 33.7%; Score 28; DB 16; Length 12;

Best Local Similarity 45.3%; Pred. No. 1.1e+02;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 4 ECKPQVTRGDV 14

II: I I I I I

Db 2 kckeavkrkev 12

RESULT 14

ID Y84806 standard; peptide; 12 AA.

XX Y84806;

AC Y84806;

XX 08-AUG-2000 (first entry)

DE Internal peptide of tumour necrosis factor inhibitory protein B1.

XX Tumour necrosis factor; TNF; TNF inhibitory protein; TIP; TIP-B1;

KW TNF-induced cell lysis; TNF-induced apoptosis; cytolytic; septic shock;

KW Chronic inflammation; arthritis; cancer; cachexia; autoimmune disease.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1

FT EP997475-A1. /note= "unspecified amino acid"

XX 03-MAY-2000.

PD 03-MAY-2000.

XX 04-DEC-1998; 98EP-0123140.

PF 04-DEC-1998; 98EP-0123140.

XX 21-SEP-1998; 98US-0157910.

PR 21-SEP-1998; 98US-0157910.

XX (HEAL-) HEALTH RES INC.

PA (HEAL-) HEALTH RES INC.

XX Berleth E, Ehrke JM, Nadadur S, Gurtoo H, Henn A, Mihich E;

PI Berleth E, Ehrke JM, Nadadur S, Gurtoo H, Henn A, Mihich E;

XX WPI: 2000-305801/27.

DR WPI: 2000-305801/27.

XX Tumour necrosis factor inhibitory protein B1 capable of inhibiting the

PT action of tumor necrosis factor upon introduction into the

PT extracellular region of cells, useful for treating e.g. chronic

PT inflammation

XX Claim 2; Page 15; 47pp; English.

PS Y84804-06 represent internal peptides of a tumour necrosis factor

CC (TNF) inhibitory protein (TIP) designated TIP-B1. The TIP-B1 protein

CC has a molecular weight of 27 kD, and which, upon introduction into

CC the extracellular region of surrounding cells, is capable of

CC inhibiting the action of TNF upon those cells. TIP-B1 is useful

CC for inhibiting the action of TNF upon a cell to ablate e.g.

CC TNF-induced cell lysis, TNF-induced apoptosis and cytolytic effects.

CC TIP-B1 can therefore be used to treat TNF-mediated diseases such

CC as chronic inflammation, arthritis, cancer (cachexia), autoimmune

CC diseases and septic shock.

XX Sequence 12 AA:

SO

Query Match 33.7%; Score 28; DB 21; Length 12;

Best Local Similarity 44.4%; Pred. No. 1.1e+02;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 PQVTRGDV 15

II: I I I I I

Db 4. pglvngdyg 12

RESULT 15

ID R95959 standard; peptide; 13 AA.

XX R95959;

AC R95959;

XX 08-AUG-1996 (first entry)

DE Heterologous protein N-terminal extension #24.

XX Signal peptide; alpha-factor; dipeptidyl aminopeptidase processing;

KW proteolysis; yeast; apocytin; tissue factor pathway inhibitor; ILGF-1;

KW protease inhibitor; insulin-like growth factor I; ILGF-II; interleukin;

KW human growth hormone; bovine growth hormone; glucagon-like peptide-1;

KW tissue plasminogen activator; glucagon; Factor VII; Factor VIII; insulin;

KW Factor XIII; platelet derived growth factor; insulin precursor.

XX Synthetic.

OS Synthetic.

XX W09535384-A1.

PN W09535384-A1.

XX 28-DEC-1995.

PD 28-DEC-1995.

XX 15-JUN-1995; 95MO-DK00250.

PF 15-JUN-1995; 95MO-DK00250.

XX 17-JUN-1994; 94DX-0000712.

PR 17-JUN-1994; 94DX-0000712.

XX

PA (NOVO ) NOVO-NORDISK AS.

XX  
PI Brandt J, Kjeldsen TB, Vad K;

XX  
DR WPI; 1996-058421/06.

XX  
PT DNA construct for expressing N-terminally extended heterologous  
PT protein in yeast - enabling higher yield of correctly processed  
PT proteins such as growth hormone, interleukin, tissue plasminogen  
PT activator and insulin

XX  
PS Example 11; Page 28; 79pp; English.

XX  
CC R87060-R87082 and R95959 represent possible N-terminal extensions for  
CC heterologous proteins (HP) in yeast. The N-terminally extended HP has a  
CC signal peptide (such as the alpha-factor signal peptide, see R87059), a  
CC leader sequence and a yeast processing site attached to its N-terminus.  
CC The DNA encoding this construct is then inserted into a recombinant  
CC expression vector which is used to transform a yeast strain capable of  
CC expressing the heterologous protein. The yeast processing site,  
CC contained within the N-terminal extension, enables the leader sequence  
CC and signal peptide to be removed. The N-terminal extension of the HP  
CC increases the fermentation yield and protects against dipeptidyl  
CC aminopeptidase processing. The extension can be cleaved off either by  
CC naturally occurring yeast proteases before purification from the culture  
CC media or by in vitro proteolysis during or subsequent to purification of  
CC the product. These constructs can be used to obtain higher yields of  
CC correctly processed proteins such as aprotinin, tissue factor pathway  
CC inhibitor, protease inhibitors, insulin-like growth factor I (IGF-I),  
CC IGF-II, human or bovine growth hormone, interleukin, tissue plasminogen  
CC activator, glucagon, glucagon-like peptide-1, Factor VII, Factor VIII,  
CC Factor XIII, platelet derived growth factor, enzymes, insulin, or an  
CC insulin precursor.

XX  
SQ Sequence 13 AA;

Query Match 33.7%; Score 28; DB 17; Length 13;

Best Local Similarity 55.6%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 AECKPOVTR 11

DB 11 : 1 : 11  
5 aeepkatr 13

Search completed: March 6, 2001, 09:48:41  
Job time: 163 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:47:08 ; Search time 12.67 Seconds  
(without alignments)  
21.259 Million cell updates/sec

Title: US-09-081-522-8

Perfect score: 83

Sequence: 1 YTAECKPQYTRGDVF 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 78116

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: Issued\_Patents\_AA.\*  
2: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/PCUS.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/Backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	15	1	US-08-210-715-8
2	83	100.0	15	1	US-08-366-665-8
3	36	43.4	9	1	US-08-421-702A-6
4	36	43.4	9	1	US-08-303-052A-6
5	36	43.4	9	1	US-08-421-696A-6
6	36	43.4	9	1	US-08-421-697A-6
7	36	43.4	9	1	US-08-421-698A-6
8	36	43.4	9	2	US-08-421-695A-6
9	36	43.4	9	4	PCT-US95-04741-6
10	30	36.1	10	3	US-08-763-458-28
11	30	36.1	10	3	US-08-763-458-29
12	29	34.9	11	4	PCT-US91-08328-10
13	28	33.7	12	1	US-08-444-231-22
14	28	33.7	12	1	US-08-152-443A-22
15	27	32.5	8	1	US-08-014-426-54
16	27	32.5	8	4	PCT-US94-01319-54
17	27	32.5	8	5	5179198-5
18	27	32.5	8	5	5521296-5
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22	27	32.5	11	3	US-08-763-458-16
23	27	32.5	14	1	US-08-325-071-70
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25	27	32.5	15	2	US-08-487-074-7
26	27	32.5	15	3	US-08-763-458-7
27	26	31.3	9	1	US-08-421-702A-53
28	26	31.3	9	1	US-08-421-702A-99

29	26	31.3	9	1	US-08-303-052A-72	Sequence 72, Appl
30	26	31.3	9	1	US-08-303-052A-99	Sequence 99, Appl
31	26	31.3	9	1	US-08-421-696A-53	Sequence 53, Appl
32	26	31.3	9	1	US-08-421-696A-99	Sequence 99, Appl
33	26	31.3	9	1	US-08-421-697A-53	Sequence 53, Appl
34	26	31.3	9	1	US-08-421-697A-99	Sequence 99, Appl
35	26	31.3	9	1	US-08-421-698A-53	Sequence 53, Appl
36	26	31.3	9	1	US-08-421-698A-99	Sequence 99, Appl
37	26	31.3	9	2	US-08-421-695A-100	Sequence 100, App
38	26	31.3	9	2	US-08-421-695A-142	Sequence 142, App
39	26	31.3	10	1	US-08-710-305-1	Sequence 1, Appl
40	26	31.3	12	3	US-08-742-243-3	Sequence 3, Appl
41	26	31.3	12	3	US-08-742-243-65	Sequence 65, Appl
42	26	31.3	12	3	US-08-742-243-66	Sequence 66, Appl
43	26	31.3	12	3	US-08-742-243-67	Sequence 67, Appl
44	26	31.3	14	3	US-08-807-992B-9	Sequence 9, Appl
45	26	31.3	14	3	US-08-807-992B-12	Sequence 12, Appl

#### ALIGNMENTS

RESULT 1  
US-08-210-715-8  
Sequence 8, Application US/08210715  
Patent No. 5753230  
GENERAL INFORMATION:  
APPLICANT: Brooks, Peter  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
INHIBITION OF ANGIOGENESIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: Office of Patent Counsel, The Scripps  
ADDRESS: Research Institute  
STREET: 10665 No. 5753230th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/210,715  
FILING DATE: 18-MAR-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOC/KET NUMBER: TSRI 419.0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (519) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
US-08-210-715-8

Query Match 100.0%; Score 83; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTAECKPOVTRGDVF 15  
| | | | | | | | | | |  
Db 1 YTAECKPOVTRGDVF 15

## RESULT 2

US-08-366-665-8  
; Sequence 8, Application US/08366665  
; Patent No. 5766591  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Peter  
; APPLICANT: Cheres, David A  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR  
; TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Office of Patent Counsel, The Scripps  
; ADDRESSEE: Research Institute  
; STREET: 10666 No. 5766591th Torrey Pines Road, TPC-8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/366.665  
FILING DATE: 30-DEC-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/210,715  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Filling, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 419.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
US-08-366-665-8

Query Match 100.0%; Score 83; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTAECKPOVTRGDVF 15  
| | | | | | | | | | |  
Db 1 YTAECKPOVTRGDVF 15

## RESULT 3

US-08-421-702A-6  
; Sequence 6, Application US/08421702A  
; Patent No. 5759996  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Soan  
; APPLICANT: Ingram, Ronald  
; APPLICANT: Mullen, Daniel  
; APPLICANT: Tschopp, Jueerg

TITLE OF INVENTION: Peptides Useful for Altering Alpha-  
; TITLE OF INVENTION: v Beta-3-Mediated Binding  
; NUMBER OF SEQUENCES: 140  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/421,702A  
FILING DATE: 12-APR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/303,052  
FILING DATE: 08-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 1480  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-6949  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-421-702A-6

Query Match 43.4%; Score 36; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VTRGDVF 15  
| | | | | | | | | | |  
Db 1 VTRGDVF 7

## RESULT 4

US-08-303-052A-5  
; Sequence 5, Application US/08303052A  
; Patent No. 5770565  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Soan  
; APPLICANT: Ingram, Ronald  
; APPLICANT: Mullen, Daniel  
; APPLICANT: Tschopp, Jueerg  
; TITLE OF INVENTION: Peptides for Reducing or Inhibiting Bone  
; TITLE OF INVENTION: Resorption  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/303,052A

FILING DATE: 08-SEP-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,316  
FILING DATE: 13-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 1132  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-303-052A-6

Query Match 43.4%; Score 36; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VTRGDVF 15  
|||||  
Db 1 VTRGDVF 7

RESULT 5  
US-08-421-696A-6  
Sequence 6, Application US/08421696A  
Patent No. 5773412  
GENERAL INFORMATION:  
APPLICANT: Cheng, Soan  
APPLICANT: Ingram, Ronald  
APPLICANT: Mullen, Daniel  
APPLICANT: Tschopp, Juerg  
TITLE OF INVENTION: Use of Peptides for Altering alpha-v  
NUMBER OF SEQUENCES: 138  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/421,696A  
FILING DATE: 12-APR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/303,052  
FILING DATE: 08-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 1479  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-421-696A-6  
Query Match 43.4%; Score 36; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VTRGDVF 15  
|||||  
Db 1 VTRGDVF 7

RESULT 6  
US-08-421-697A-6  
Sequence 6, Application US/08421697A  
Patent No. 5792745  
GENERAL INFORMATION:  
APPLICANT: Cheng, Soan  
APPLICANT: Ingram, Ronald  
APPLICANT: Mullen, Daniel  
APPLICANT: Tschopp, Juerg  
TITLE OF INVENTION: Use of Peptides for Altering Bone  
RESORPTION  
NUMBER OF SEQUENCES: 138  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/421,697A  
FILING DATE: 12-APR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,316  
FILING DATE: 13-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/303,052  
FILING DATE: 08-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 1412  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-421-697A-6

Query Match 43.4%; Score 36; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VTRGDVF 15  
|||||  
Db 1 VTRGDVF 7

RESULT 7  
US-08-421-698A-6

Sequence 6, Application US/08421698A  
Patent No. 5807819  
GENERAL INFORMATION:  
APPLICANT: Cheng, Soan  
APPLICANT: Ingram, Ronald  
APPLICANT: Mullen, Daniel  
APPLICANT: Tschopp, Juerg  
TITLE OF INVENTION: Peptides useful for Altering Bone  
RESORPTION  
NUMBER OF SEQUENCES: 138  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/421,698A  
FILING DATE: 12-APR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/303,052  
FILING DATE: 08-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 1481  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-421-698A-6

Query Match 43.4%; Score 36; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 VTRGDVF 15  
| | | | |  
DB 1 VTRGDVF 7

RESULT 8  
US-08-421-695A-6  
Sequence 6, Application US/08421695A  
Patent No. 5849865  
GENERAL INFORMATION:  
APPLICANT: Cheng, Soan  
APPLICANT: Ingram, Ronald  
APPLICANT: Mullen, Daniel  
APPLICANT: Tschopp, Juerg  
TITLE OF INVENTION: Peptides for Altering Bone Resorption,  
Angiogenesis and Restenosis  
NUMBER OF SEQUENCES: 143  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/421,695A  
FILING DATE: 12-APR-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 1478  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: circular  
MOLECULE TYPE: peptide  
US-08-421-695A-6

Query Match 43.4%; Score 36; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 VTRGDVF 15  
| | | | |  
DB 1 VTRGDVF 7

RESULT 9  
PCT-US95-04741-6  
Sequence 6, Application PC/TUS9504741  
GENERAL INFORMATION:  
APPLICANT: La Jolla Cancer Research Foundation  
TITLE OF INVENTION: Peptides for Reducing or Inhibiting Bone  
RESORPTION, Angiogenesis and Restenosis  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04741  
FILING DATE: 12-APR-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,316  
FILING DATE: 13-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/303,052  
FILING DATE: 08-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Imbra, Richard J.  
REGISTRATION NUMBER: 37,643  
REFERENCE/DOCKET NUMBER: FP-LA 1476  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:



LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US95-04741-6

Query Match 43.4%; Score 36; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YTRGDVF 15  
:|||||  
Db 1 YTRGDVF 7

RESULT 10  
US-08-763-458-28  
Sequence 28, Application US/08763458  
Patent No. 6117839  
GENERAL INFORMATION:  
APPLICANT: TAM, Cheryl Shing  
TITLE OF INVENTION: BONE STIMULATING FACTOR  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 75/08/763,458  
FILING DATE: 11-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/467,074  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 79997/118  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ. ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-763-458-28

Query Match 36.1%; Score 30; DB 3; Length 10;  
Best Local Similarity 83.3%; Pred. No. 37;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTRAECK 6  
:|||||  
Db 5 YTRAECK 10

RESULT 11  
US-08-763-458-29  
Sequence 29, Application US/08763458  
Patent No. 6117839

GENERAL INFORMATION:  
APPLICANT: TAM, Cheryl Shing  
TITLE OF INVENTION: BONE STIMULATING FACTOR  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/763,458  
FILING DATE: 11-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/467,074  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 79997/118  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ. ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-763-458-29

Query Match 36.1%; Score 30; DB 3; Length 10;  
Best Local Similarity 83.3%; Pred. No. 37;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTRAECK 5  
:|||||  
Db 5 YTRAECK 10

RESULT 12  
PCT-US91-08328-10  
Sequence 10, Application PC/TUS9108328  
GENERAL INFORMATION:  
APPLICANT: Ruggeri, Zaverio M.  
TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN  
STREET: 345 Park Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/7591/08328  
FILING DATE: 19911107

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/610,363  
FILING DATE: 07-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: MOTOZ, Eugene  
REGISTRATION NUMBER: 25,237  
REFERENCE/DOCKET NUMBER: 1198 4079PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)758-4800  
TELEFAX: (212)751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Cross-Links  
LOCATION: 2..11  
OTHER INFORMATION: /note= "Multimers of sequence  
OTHER INFORMATION: linked by interchain disulfide bonds at Cys  
OTHER INFORMATION: residues"  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: US 4,683,291  
FILING DATE: 28-OCT-1985  
PUBLICATION DATE: 28-JUL-1987  
DOCUMENT INFORMATION:  
DOCUMENT NUMBER: US B1 4,683,291  
FILING DATE: 28-OCT-1985  
PUBLICATION DATE: 03-JUL-1990  
PCT-US91-08328-10

Query Match 34.9%; Score 29; DB 4; Length 11;  
Best Local Similarity 50.0%; Pred. No. 59;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 5 CKPOVTRGDV 14  
: : : : :  
Db 2 CRRRRRGDV 11

RESULT 13  
US-08-444-231-22  
Sequence 22, Application US/08444231  
Patent No. 5652210  
GENERAL INFORMATION:  
APPLICANT: BARR, PHILIP J.  
APPLICANT: SHAPIRO, JOHN P.  
APPLICANT: KIEFER, MICHAEL C.  
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,231  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/152,443  
FILING DATE: 15-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: LEHNHARDT, SUSAN K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 23647-20006.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-444-231-22

Query Match 33.7%; Score 28; DB 1; Length 12;  
Best Local Similarity 45.5%; Pred. No. 93;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 4 ECKPQVTRGDV 14  
: : : : :  
Db 2 CKKEVYKREY 12

RESULT 14  
US-08-152-443A-22  
Sequence 22, Application US/08152443A  
Patent No. 5663070  
GENERAL INFORMATION:  
APPLICANT: BARR, PHILIP J.  
APPLICANT: SHAPIRO, JOHN P.  
APPLICANT: KIEFER, MICHAEL C.  
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/152,443A  
FILING DATE: 15-NOV-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: LEHNHARDT, SUSAN K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 23647-20006.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-152-443A-22

Query Match 33.7%; Score 28; DB 1; Length 12;  
Best Local Similarity 45.5%; Pred. No. 93;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 ECKPQVTRGDV 14  
:|:|:|:|  
Db 2 KCKEYKRRREV 12

## RESULT 15

US-08-014-426-54  
; Sequence 54, Application US/08014426  
; Patent No. 5512435  
; GENERAL INFORMATION:  
; APPLICANT: Renschler, Markus F.  
; APPLICANT: Levy, Ronald  
; APPLICANT: Bhall, Ramesh  
; APPLICANT: Dower, William  
; TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE  
; TITLE OF INVENTION: PEPTIDES  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/014,426  
; FILING DATE: 05-FEB-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 5490A-204  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: NO  
US-08-014-426-54

Query Match 32.5%; Score 27; DB 1; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTAECK 6  
:|:|:|  
Db 2 WTADCK 7

Search completed: March 6, 2001, 09:48:57  
Job time: 109 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 6, 2001, 09:47:33 ; Search time 13.92 Seconds  
(without alignments)  
73.169 Million cell updates/sec

Title: US-09-081-522-8

Perfect score: 83  
Sequence: 1 YRAECKPQVTRGDVF 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_66:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	39.8	11	2	S42449 anti protein - pha
2	25	30.1	9	2	B46250 alpha-adaptin - bo
3	22	26.5	10	1	RHLMG5 gonadoliberin - bo
4	22	26.5	10	2	S70721 heat shock protein
5	22	26.5	14	2	PH0765 T-cell receptor be
6	21.5	25.9	15	2	A35389 urase (EC 3.5.1.5
7	21	25.3	11	2	S66606 quinoline 2-oxidor
8	21	25.3	12	2	PH1587 Ig H chain V-D-J r
9	21	25.3	14	2	PC7075 gamma-galactosylase
10	21	25.3	15	2	P00017 terminal protein -
11	21	25.3	15	2	A60763 endo-1,3-beta-glyc
12	20	24.1	11	2	S60354 retinal oxidase -
13	20	24.1	12	1	UCGM2 utrotenin II - for
14	20	24.1	12	2	S42765 utrotenin II - tel
15	20	24.1	14	2	PC4271 neurotensin-relate
16	20	24.1	15	2	A28497 milk band B protei
17	20	24.1	15	2	C61511 epidermal growth f
18	20	24.1	15	4	S08301 hypothetical MN1/T
19	20	24.1	15	4	I38031 kidney and bladder
20	19	22.9	9	2	G58502 antibiotic GE2270
21	19	22.9	13	2	A61210 Ig H chain V-D-J r
22	19	22.9	14	2	PH1594 fil3 ligand isofor
23	19	22.9	15	2	I78838 hypothetical pepti
24	18	21.7	7	4	I55382 low density lipopr
25	18	21.7	11	2	S45386 S-allele-associate
26	18	21.7	14	2	S39932 lutropin beta chn
27	18	21.7	14	2	B61309 bleomycin-binding
28	18	21.7	15	2	S68731 protein OF200051 -
29	18	21.7	15	2	PA0088

30	18	21.7	15	2	S29487 GTP-binding protei
31	17	20.5	8	2	I57532 gene Tnrlow prote
32	17	20.5	10	1	XAV16B angiotensin-conver
33	17	20.5	10	2	S66214 cartilage oligomer
34	17	20.5	11	1	SPHO substance P - hors
35	17	20.5	11	1	A60654 alcohol dehydrogen
36	17	20.5	11	2	S65196 bradykinin-potentl
37	17	20.5	11	2	C37196 bradykinin-potentl
38	17	20.5	11	2	D37196 enterotoxin C-1 -
39	17	20.5	12	2	A60757 tremetoxin a-13 -
40	17	20.5	13	1	UTG3 alpha-2 collagen
41	17	20.5	13	2	I50173 chaperone, TCPI-re
42	17	20.5	14	2	S33803 collagen alpha cha
43	17	20.5	14	2	S23376 beta-granin - rat
44	17	20.5	14	2	A23996 acid phosphatase (
45	17	20.5	15	2	A56963

## ALIGNMENTS

RESULT 1  
S42449  
anti protein - phage p7  
C:Species: Phage p7  
C:Date: 07-Sep-1994 #sequence\_revision 26-May-1995 #text\_Change 08-Oct-1999  
C:Accession: S42449  
R:Clifton, M.; Schuster, H.  
Cell 62, 591-598, 1990  
A:Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.  
A:Reference number: S42448; MUID:90335968  
A:Accession: S42449  
A:Status: preliminary; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-11 <CIT>  
A:Cross-references: ENEM:M35139; NID:9215705; PIDN:AAA32437.1; PID:9215707

Query Match 39.8% Score 33; DB 2; Length 11;  
Best Local Similarity 65.7% Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 KPOVTRGDV 14  
|||  
DB 3 KPIVTRNDI 11

RESULT 2  
B46250  
alpha-adaptin - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_Change 05-Apr-1995  
C:Accession: B46250  
R:Titmerman, A.P.; Mayrleitter, M.M.; Lukas, T.J.; Chadwick, C.C.; Saito, A.; Wattersc  
Proc. Natl. Acad. Sci. U.S.A. 89, 8976-8980, 1992  
A:Title: Inositol polyphosphate receptor and clathrin assembly protein AP-2 are relat  
A:Reference number: A46250; MUID:93028388  
A:Accession: B46250  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <TIM>

Query Match 30.1% Score 25; DB 2; Length 9;  
Best Local Similarity 57.1% Pred. No. 2e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 POWTRGD 13  
|:|:|  
DB 1 PAVSRGD 7

RESULT 3

## RHLMS

gonadoliberin - sea lamprey  
N:Alternate names: gonadotropin releasing hormone (GNRH)

C:Species: Petromyzon marinus (sea lamprey)

C>Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 18-Mar-1997

C:Accession: A01412

R:Sherwood, N.M.; Sower, S.A.; Marshak, D.R.; Fraser, B.A.; Brownstein, M.J.

J. Biol. Chem. 261, 4812-4819, 1986

A:Title: Primary structure of gonadotropin-releasing hormone from lamprey brain.

A:Reference number: A01412; MUID:86158192

A:Accession: A01412

A:Molecule type: Protein

A:Residues: 1-10 <SHE>

C:Comment: This hormone was isolated from the brain.

C:Superfamily: gonadoliberin

C:Keywords: amidated carboxyl end; hormone; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match

Best Local Similarity 26.5%; Score 22; DB 1; Length 10;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTAECKP 7

DB 3 YSLEWKP 9

RESULT 4

heat shock protein C62.5 homolog - Salmonella typhimurium (fragment)

N:Alternate names: high temperature protein G

C:Species: Salmonella typhimurium

C>Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998

C:Accession: S70721

R:Qi, S.Y.; Li, Y.; Sztybel, A.; Giles, I.G.; Molr, A.; O'Connor, C.D.

Mol. Microbiol. 17, 523-531, 1995

A:Title: Salmonella typhimurium responses to a bactericidal protein from human neutrophils

A:Reference number: S70719; MUID:96100451

A:Accession: S70721

A:Molecule type: protein

A:Residues: 1-10 <QIS>

A:Experimental source: strain SL1344

C:Keywords: ATP binding; heat shock; molecular chaperone;

Query Match

Best Local Similarity 26.5%; Score 22; DB 2; Length 10;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 KPOVTRG 12

DB 2 KGOETRG 8

RESULT 5

PH0765

T-cell receptor beta chain (H1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999

C:Accession: PH0765

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-1

allelic exclusion and antigen-specific repertoire.

## Query Match

Best Local Similarity 26.5%; Score 22; DB 2; Length 14;

Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 CKPQVTRGD 13

DB 1 CASSARD 9

RESULT 6

A35389

urease (EC 3.5.1.5) 63K chain - Morganella morganii (fragment)

C:Species: Morganella morganii

C>Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 23-Jun-1993

C:Accession: A35389

R:Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.

J. Bacteriol. 172, 3073-3080, 1990

A:Title: Morganella morganii urease: purification, characterization, and isolation of

A:Reference number: A35389; MUID:90264298

A:Accession: A35389

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <HUN>

C:Keywords: hydrolase

Query Match

Best Local Similarity 25.9%; Score 21.5; DB 2; Length 15;

Matches 5; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

OY 7 POWTR---GDYF 15

DB 1 PDISRGEGSLF 12

RESULT 7

S66506

guinoline 2-oxidoreductase alpha chain - Comamonas testosteroni (fragment)

C:Species: Comamonas testosteroni

C>Date: 15-Feb-1987 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C:Accession: S66506

R:Schach, S.; Tshisuka, B.; Fetzner, S.; Lingsens, F.

Eur. J. Biochem. 232, 536-544, 1995

A:Title: Guinoline 2-oxidoreductase and 2-oxo-1,2-dihydroguinoline 5,6-dioxygenase fr

A:Reference number: S66506; MUID:96035889

A:Accession: S66506

A:Molecule type: protein

A:Residues: 1-11 <SCH>

A:Experimental source: strain 63

Query Match

Best Local Similarity 25.3%; Score 21; DB 2; Length 11;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 AECYPO 8

DB 6 AELKPR 11

RESULT 8

PH1587

Ig H chain V-D-J region (wild-type clone 11) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C:Accession: PH1587

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Molecule type: DNA  
A:Residues: 1-12 <LEV>  
A:Experimental source: bone marrow pre-B lymphocyte  
C:Keywords: immunoglobulin

Query Match 25.3%; Score 21; DB 2; Length 12;  
Best Local Similarity 60.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 11 RGDVF 15  
|||:  
DB 4 RGDLY 8

RESULT 9  
PC7075  
guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C:Accession: PC7075  
R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;  
Electrophoresis 21, 1853-1871, 2000  
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of  
A:Reference number: PC7072  
A:Accession: PC7075  
A:Molecule type: protein  
A:Residues: 1-14 <TSD>  
A:Experimental source: strain C57BL/6Cr Slc, male; brain, striatum  
C:Keywords: brain; phosphorus-oxygen lyase

Query Match 25.3%; Score 21; DB 2; Length 14;  
Best Local Similarity 42.9%; Pred. No. 2e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 9 VTRGDVF 15  
:|:|:  
DB 8 IPRGEVF 14

RESULT 10  
P00017  
terminal protein - phage M2 (fragment)  
C:Species: phage M2  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Sep-1999  
C:Accession: P00017  
R:Matsumoto, K.; Takano, H.; Kim, C.I.; Hirokawa, H.  
Gene 84, 247-255, 1989  
A:Title: Primary structure of bacteriophage M2 DNA polymerase: conserved segments within  
A:Reference number: J00161; MUID:90128268  
A:Accession: P00017  
A:Molecule type: DNA  
A:Residues: 1-15 <MAT>  
A:Cross-references: GB:M33144; NID:G215507; PID:AAA32367.1; PID:G215508  
A:Gene: E  
C:Superfamily: phage PZA terminal protein

Query Match 25.3%; Score 21; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 RGDV 14  
|||:  
DB 5 RGDV 8

RESULT 11  
A60763  
endo-1,3-beta-glucanase (EC 3.2.1.-), 68k - Bacillus circulans (strain WL-12) (fragment)  
C:Species: Bacillus circulans

C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 07-May-1999  
C:Accession: A60763  
R:Fiske, M.J.; Tobey-Fincher, K.L.; Fuchs, R.L.  
J. Gen. Microbiol. 136, 2377-2383, 1990  
A:Title: Cloning of two genes from Bacillus circulans WL-12 which encode 1,3-beta-glu  
A:Reference number: A60763; MUID:91178514  
A:Accession: A60763  
A:Molecule type: protein  
A:Residues: 1-15 <FIS>  
C:Comment: This bacillus produces up to six different 1,3-beta-glucanases for growth  
C:Keywords: glycosidase; hydrolase

Query Match 25.3%; Score 21; DB 2; Length 15;  
Best Local Similarity 44.4%; Pred. No. 2.1e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 PQRVGRDV 15  
|||:  
DB 3 PVRSMERY 11

RESULT 12  
S60354  
retinal oxidase - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S60354  
R:Huang, D.Y.; Ichikawa, Y.  
Biochim. Biophys. Acta 1243, 431-435, 1995  
A:Title: Identification of essential lysyl and cysteinyl residues, and the amino acid  
A:Reference number: S60354; MUID:95244596  
A:Accession: S60354  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <HDV>

Query Match 24.1%; Score 20; DB 2; Length 11;  
Best Local Similarity 42.9%; Pred. No. 2.3e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 YTAECKP 7  
:|:|:  
DB 5 HTXGCKP 11

RESULT 13  
U06M2  
urotensin II - long-jawed mudsnaker  
C:Species: Gilllichthys mirabilis (long-jawed mudsnaker)  
C:Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 15-Oct-1996  
C:Accession: A01409  
R:Pearson, D.; Shively, J.E.; Clark, B.R.; Gesschwind, I.I.; Barkley, M.; Nishioke, R.  
Proc. Natl. Acad. Sci. U.S.A. 77, 5021-5024, 1980  
A:Title: Urotensin II: a somatostatin-like peptide in the caudal neurosecretory syste  
A:Reference number: A01409; MUID:81054904  
A:Accession: A01409  
A:Molecule type: protein  
A:Residues: 1-12 <PEA>  
A:Note: the proposed sequence was confirmed by synthesis of a peptide with the same s  
C:Comment: Urotensin II is found in the teleost caudal neurosecretory system and is i  
C:Superfamily: urotensin II  
C:Keywords: neuropeptide; osmoregulation  
F:6-11/Disulfide bonds: #status experimental

Query Match 24.1%; Score 20; DB 1; Length 12;  
Best Local Similarity 75.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 TAEC 5  
||:|

Db 3 TADC 6

## RESULT 14

S42765  
urotensin II - telostean fish  
C:Species: telostean fish  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 05-Dec-1997  
C:Accession: S42765  
R:Bhaskaran, R.; Arunkumar, A.I.; Yu, C.  
Biochim. Biophys. Acta 1199, 115-122, 1994  
A:Title: NMR and dynamical simulated annealing studies on the solution conformation of u  
A:Reference number: S42765; MUID:94169160  
A:Accession: S42765  
A:Molecule type: protein  
A:Residues: 1-12 <BHA>  
C:Superfamily: urotensin II  
C:Keywords: neuropeptide; osmoregulation  
F:6-11/Product: urotensin II #status experimental <MAT>

## Query Match

Best Local Similarity 24.1%; Score 20; DB 2; Length 12;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 TAEC 5

Db 3 TADC 6

## RESULT 15

PC4271  
unidentified GR310007 protein - rice (fragment)  
C:Species: Oryza sativa (rice)  
C:Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 18-Jul-1997  
C:Accession: PC4271  
R:Kawakami, T.; Kano, M.; Chen, M.C.; Tsugita, A.  
submitted to JIPID, April 1997  
A:Reference number: PC4267  
A:Accession: PC4271  
A:Molecule type: protein  
A:Residues: 1-14 <KAW>

## Query Match

Best Local Similarity 24.1%; Score 20; DB 2; Length 14;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 7 PQVTRGD 13

Db 1 PGLTIGD 7

Search completed: March 6, 2001, 09:49:16  
Job time: 103 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 6, 2001, 09:48:43 ; Search time 8.42 Seconds

(Without alignments)  
57.531 Million cell updates/sec

Title: US-09-081-522-8

Sequence: 1 Y7AECKPQVTRGDVF 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 705

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	30.1	15	1 UC19_MAIZE	P80625 zea mays (m
2	22	26.5	10	1 GON1_PETMA	P04378 petromyzon
3	22	26.5	13	1 YPE2_LACTIC	P42021 lactococcus
4	21.5	25.9	15	1 URE1_MORMO	P17337 morganelia
5	21	25.3	15	1 OZOA_CONTE	P80454 comanonas t
6	21	25.3	15	1 TERW_BPM2	P19897 bacterioph
7	20	24.1	12	1 UR2_GILMI	P01147 gillichthys
8	20	24.1	12	1 UN02_PIPNS	P81022 polyodon sp
9	19	22.9	9	1 RS11_SALTY	P81667 pinus pinas
10	19	22.9	13	1 PED1_HYDAT	P80578 hydra atten
11	17.5	21.1	9	1 OXIT_RAUCI	P42994 raja clavat
12	17	20.5	10	1 BPP2_BOTIN	P01022 bothrops ja
13	17	20.5	11	1 BPP3_BOTIN	P30423 bothrops in
14	17	20.5	11	1 BPP4_BOTIN	P30424 bothrops in
15	17	20.5	11	1 TKNA_HO3SE	P01290 equus cabal
16	17	20.5	13	1 TAL3_TREME	P01370 tremella me
17	17	20.5	13	1 UN12_CLOPA	P81353 clostridium
18	17	20.5	14	1 TAT_HV1W2	P12509 human immun
19	17	20.5	14	1 TAT_HV1W2	P12511 human immun
20	17	20.5	15	1 CBPB_PROAT	P19628 protopteris
21	17	20.5	15	1 CXAL_CONGE	P01871 conus geogr
22	17	19.3	7	1 EARL_HELTI	P41871 heliosoma tr
23	16	19.3	9	1 ISOT_CIFCA	P42993 cyprinus ca
24	16	19.3	9	1 UP06_HUMAN	P30092 homo sapien
25	16	19.3	10	1 TKSL_AEDAE	P42634 aedes aegyp
26	16	19.3	10	1 TKSL_AEDAE	P42635 aedes aegyp
27	16	19.3	11	1 COR2_PERAM	P11496 petriplaneta
28	16	19.3	13	1 CXAL_CONST	P15471 conus strita
29	16	19.3	14	1 SMS_MYOSC	P20750 myoxocephal
30	16	19.3	14	1 SMS_ALIMI	P1885 alligator m
31	16	19.3	15	1 ESTB_SCHGA	P01011 schizaphis
32	16	19.3	15	1 UC30_MAIZE	P80636 zea mays (m
33	16	19.3	15	1 UC30_MAIZE	P80636 zea mays (m

34	15	18.1	7	1 FAR4_PANRE	P41875 panagrellius
35	15	18.1	10	1 AMPN_HELAM	P81721 helicoverpa
36	15	18.1	10	1 BPP2_BOTIN	P30422 bothrops in
37	15	18.1	10	1 FAR4_MYTED	P42560 mytilus edu
38	15	18.1	10	1 UHA3_HUMAN	P40930 homo sapien
39	15	18.1	10	1 UP05_HUMAN	P30091 homo sapien
40	15	18.1	12	1 TKN_KASSE	P08611 kassina sen
41	15	18.1	12	1 UR2A_CATCO	P04558 catostomus
42	15	18.1	12	1 V14K_MSSV	P82006 white spot
43	15	18.1	13	1 CXA2_CONGE	P01520 conus geogr
44	15	18.1	13	1 CXA1_CONST	P28878 conus strita
45	15	18.1	14	1 CXA1_CONCN	P56973 conus conso

#### ALIGNMENTS

RESULT 1	UC19_MAIZE	STANDARD;	PRT;	15 AA.
AC	P80625:			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 406)			
DE	(FRAGMENT).			
OS	zea mays (maize).			
OC	Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE-COLEOPTILE;			
RA	Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,			
RA	Pennollet J.-C., Zivy M., de Vienne D.,			
RT	"The maize two dimensional gel protein database: towards an integrated			
RT	genome analysis program."			
RT	Theor. Appl. Genet. 93:997-1003(1996).			
CC	-I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN			
CC	PROTEIN IS: 5.6, ITS MW IS: 18.4 KDA.			
DR	MAIZE-2DPAGE; P80625; COLEOPTILE.			
DR	MAIZEDB; 123951; ..			
FT	NON_TER	1		
FT	NON_TER	15		
SO	SEQUENCE	15 AA; 1672 MW; 1CF69D4DA8737F9D CRC64;		

  

Query Match	30.1%;	Score 25;	DB 1;	Length 15;
Best Local Similarity	55.6%;	Pred. No. 1.6e+02;		
Matches	5;	Conservative	0;	Mismatches 4;
			Indels	0;
			Gaps	0;

  

QY	2 TAECKPQVT 10			
DB	7 TYGCSPPVT 15			

  

RESULT 2	GON1_PETMA	STANDARD;	PRT;	10 AA.
ID	GON1_PETMA			
AC	P04378:			
DT	20-MAR-1987 (Rel. 04, Created)			
DT	20-MAR-1987 (Rel. 04, Last sequence update)			
DT	01-JUN-1994 (Rel. 29, Last annotation update)			
DE	GONADOLIBERIN I (GONADOTROPIN-RELEASING HORMONE I) (GNRH-I)			
DE	(LUTALIN I).			
OS	Petromyzon marinus (Sea lamprey).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Hyperoartia;			
OC	Petromyzontiformes; Petromyzontidae; Petromyzon.			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE-BRAIN;			
RX	MEDLINE-86163192; Pubmed-3514603;			
RA	Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;			
RT	"Primary structure of gonadotropin-releasing hormone from lamprey			

RT brain.";  
 RT J Biol Chem. 261:4812-4819(1996).  
 CC -1- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND  
 CC FOLLICLE-STIMULATING HORMONES.  
 CC -1- SIMILARITY: BELONGS TO THE GNRH FAMILY.  
 DR PIR: A01412; RHLMS.  
 DR INTERPRO: IPR002012; .  
 DR PFAM: PF00446; GNRH; 1.  
 DR PROSITE: PS00473; GNRH; 1.  
 KM Hormone; Amidation; Hypothalamus.  
 FT MOD\_RSS 10 10 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RSS 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA: 1244 MW: 1E4B36237B1735AB CRC64;  
 Query Match 26.5%; Score 22; DB 1; Length 10;  
 Best Local Similarity 57.18; Pred. No. 3.7e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 YTAECKP 7  
 1: | | | |  
 3 YSLEMKP 9  
 Db 3 YSLEMKP 9  
 RESULT 3  
 ID TYPE2 LACLC STANDARD; PRT; 13 AA.  
 AC PA2021;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE HYPOPHYSICAL PROTEIN IN PEPT 5/REGION (ORF2) (FRAGMENT).  
 OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).  
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 CC Lactococcus.  
 CC [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=94245610; Pubmed=8188586;  
 RA Mierau I., Haandrikman A.J., Veltrop O., Tan P.S.T., Leenhouts K.L.,  
 RA Koning W.N., Venema G., Kok J.;  
 RT "Tripeptidase gene (pept) of Lactococcus lactis: molecular cloning  
 RT and nucleotide sequencing of pept and construction of a chromosomal  
 RT deletion mutant.";  
 RL J. Bacteriol. 176:2854-2861(1994).  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; L27596; AAA20625.1; .  
 DR Hypothetical protein.  
 KW NON\_TER 1  
 FT SEQUENCE 13 AA: 1392 MW: 3671D53271B459D7 CRC64;  
 Query Match 26.5%; Score 22; DB 1; Length 13;  
 Best Local Similarity 33.3%; Pred. No. 4.8e+02;  
 Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 2 TAECKPQVTRGD 13  
 1: | | | | | | | | | | | | | | | |  
 1 TTAIEPFISLGD 12  
 Db 1 TTAIEPFISLGD 12  
 RESULT 4  
 ID UREL\_MORMO STANDARD; PRT; 15 AA.  
 AC P17337;  
 DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE URASE ALPHA SUBUNIT (EC 3.5.1.5) (URASE AMIDOHYDROLASE) (URASE 63 KDA  
 DE SUBUNIT) (FRAGMENT).  
 GN UREC.  
 OS Morganella morganii (Proteus morganii).  
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 CC Morganella.  
 RN [1]  
 RP MEDLINE=90264298; Pubmed=2345135;  
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;  
 RT "Morganella morganii urease: purification, characterization, and  
 RT isolation of gene sequences.";  
 RL J. Bacteriol. 172:3073-3080(1990).  
 CC -1- CATALYTIC ACTIVITY: UREA + H(2)O = CO(2) + 2 NH(3).  
 CC -1- COFACTOR: EACH CHAIN BINDS TWO NICKEL IONS.  
 CC -1- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE URASE FAMILY.  
 DR PIR: A35389; A35389.  
 DR INTERPRO: IPR001924; .  
 DR PROSITE: PS00145; URASE\_2; PARTIAL.  
 DR PROSITE: PS01120; URASE\_1; PARTIAL.  
 KM Hydroxase; Metal-binding; Nickel.  
 FT NON\_TER 15  
 FT SEQUENCE 15 AA: 1550 MW: 09E27AA54241687B CRC64;  
 Query Match 25.9%; Score 21.5; DB 1; Length 15;  
 Best Local Similarity 41.7%; Pred. No. 6.9e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 3; Gaps 1;  
 QY 7 POWTR--GDVF 15  
 1: | | | | | | | | | | | | | | | |  
 1 PQISRGEGGLF 12  
 Db 1 PQISRGEGGLF 12  
 RESULT 5  
 ID Q20A\_COMTE STANDARD; PRT; 11 AA.  
 AC P80464;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE QUINOLINE 2-OXIDOREDUCTASE, ALPHA CHAIN (EC 1.-.-.-) (FRAGMENT).  
 OS Comamonas testosteroni (Pseudomonas testosteroni).  
 CC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.  
 CC [1]  
 RN SEQUENCE.  
 RP STRAIN=63;  
 RX MEDLINE=96035889; Pubmed=7556204;  
 RA Schach S., Tshisuka B., Fetzner S., Lingens F.;  
 RT "Quinolone 2-oxidoreductase and 2-oxc-1,2-dihydroquinoline 5,6-  
 RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in  
 RT quinoline and 3-methylquinoline degradation.";  
 RL Eur. J. Biochem. 232:536-544(1995).  
 CC -1- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-  
 CC 1,2-DIHYDROQUINOLINE.  
 CC -1- COFACTOR: FAD AND MOLYBDENUM.  
 CC -1- PATHWAY: FIRST STEP IN THE DEGRADATION OF QUINOLINE AND  
 CC (3-METHYL-)-QUINOLINE.  
 CC -1- SUBUNIT: HETEROHOMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND  
 CC TWO GAMMA CHAINS (PROBABLE).  
 KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.  
 FT NON\_TER 11  
 FT SEQUENCE 11 AA: 1213 MW: 869094322B1DC2CA CRC64;  
 Query Match 25.3%; Score 21; DB 1; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 6.2e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 AECKPQ 8

Db 6 AELKPR 11

RESULT 6  
TERM\_BP2 STANDARD: PRT: 15 AA.

AC P19897;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE DNA TERMINAL PROTEIN (PROTEIN GP3) (FRAGMENT).  
GN 3 OR E.  
OS Bacteriophage M2.  
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.

RP SEQUENCE FROM N.A.  
RX MEDLINE-90128268; PubMed-2515115;  
RA Matsumoto K., Takano H., Kim C.I., Hirokawa H.;  
RT "Primary structure of bacteriophage M2 DNA polymerase: conserved  
RT segments within protein-priming DNA polymerases and DNA polymerase I  
RT of Escherichia coli.";  
RL Gene 84:247-255(1989).

CC -!- FUNCTION: DNA TERMINAL PROTEIN IS LINKED TO THE 5' ENDS OF  
CC BOTH STRANDS OF THE GENOME THROUGH A PHOSPHODIESTER BOND BETWEEN  
CC THE BETA-HYDROXYL GROUP OF A SERINE RESIDUE AND THE 5'-PHOSPHATE  
CC OF THE TERMINAL DEOXYADENYLATE. THIS PROTEIN IS ESSENTIAL FOR DNA  
CC REPLICATION AND IS INVOLVED IN THE PRIMING OF DNA ELONGATION.

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CC or send an email to [license@sib.ch](mailto:license@sib.ch)).

DR EMBL: M3144; AAA32367.1; -  
DR PIR: P00017; P00017.  
KW Early protein: DNA replication; DNA priming;  
KM Covalent protein-DNA linkage.

FT SITE 1 1  
FT NON\_TER 1 1  
SQ SEQUENCE 15 AA: 1797 MW: D3CBAFF8759DEA06 CRC64;

Query Match 25.3%; Score 21; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 RGDV 14  
Db 5 RGDV 8

RESULT 7  
ID UR2\_GILMI STANDARD: PRT: 12 AA.

AC P01147;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE UROTENSIN II (U-II) (UII).  
OS Gillichthys mirabilis (Long-jawed mudsucker).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorphae; Acanthopterygii; Perciformes; Gobioidae;  
OC Gobiidae; Gillichthys.

RP SEQUENCE.  
RX MEDLINE-81054904; PubMed-6107911;  
RA Pearson D., Shively J.E., Clark B.R., Geschwind I.I., Barkley M.,  
RA Nishio R., Bern H.A.;

RT "Urotensin II: a somatostatin-like peptide in the caudal  
RT neurosecretory system of fishes."  
RL Proc. Natl. Acad. Sci. U.S.A. 77:5021-5024(1980).

CC -!- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY  
CC SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A  
CC CORTICOTROPIN-RELEASING FACTOR.

CC -!- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.  
DR PIR: A01409; UOGM2.  
DR INTERPRO: IPR001483; -  
DR PFAM: PF02083; Urotensin\_II; 1.  
DR PROSITE: PS00984; UROTENSIN\_II; 1.

KW Hormone.  
FT DISULFID 6 11  
SQ SEQUENCE 12 AA: 1364 MW: 968BF982679CEBA CRC64;

Query Match 24.1%; Score 20; DB 1; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 TAEC 5  
Db 3 TADC 6

RESULT 8  
ID UR2\_POLSP STANDARD: PRT: 12 AA.

AC P81022;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE UROTENSIN II (U-II) (UII).

OS Polyodon spathula (North American paddlefish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Chondrostei; Acipenseriformes; Polyodontidae;  
OC Polyodon.

RP SEQUENCE FROM N.A.  
RC TISSUE-SPINAL CORD;  
RX MEDLINE-96051494; PubMed-8536944;  
RA Waugh D., Youson J., Mims S.D., Sower S., Conlon J.M.;

RT "Urotensin II from the river lamprey (Lampetra fluviatilis), the sea  
RT lamprey (Petromyzon marinus), and the paddlefish (Polyodon  
RT spathula).";  
RL Gen. Comp. Endocrinol. 99:323-332(1995).

CC -!- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A  
CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH  
CC MUSCLE STIMULATION.

CC -!- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.  
DR INTERPRO: IPR001483; -  
DR PFAM: PF02083; Urotensin\_II; 1.  
DR PROSITE: PS00984; UROTENSIN\_II; 1.

KW Hormone.  
FT DISULFID 6 11  
SQ SEQUENCE 12 AA: 1410 MW: 7551E9DBB879CEBB CRC64;

Query Match 24.1%; Score 20; DB 1; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 TAEC 5  
Db 3 TSEC 6

RESULT 9  
ID UN02\_PINPS STANDARD: PRT: 13 AA.

AC P81667;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update) \*  
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDES (N55) (FRAGMENTS).  
 OS Pinus pinaster (Maritime pine).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 CC Coniferopsida; Coniferales; Pinaceae; Pinus.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=NEEDLE.  
 RX MEDLINE=99274088; PubMed=10344291.  
 RA Costa P., Plomieu C., Bauw G., Dubos C., Bahman N., Kremer A.,  
 RT Frigerio J.-M., Plomieu C.;  
 RT "Separation and characterization of needle and xylem maritime pine  
 proteins.";  
 RL Electrophoresis 20:1098-1108(1999).  
 CC -1- INDUCTION: BY WATER-STRESS.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.4, ITS MW IS: 43 KDA.  
 FT NON-TER 1 1  
 FT NON-CONS 7 8  
 FT NON-TER 13 13  
 FT SEQUENCE 13 AA; 1559 MW; 966B5A43EF94B411 CRC64;  
 SQ

Query Match 24.1%; Score 20; DB 1; Length 13;  
 Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 10 TRGVNF 15  
 1 1  
 DB 6 TRDNVF 11

RESULT 10  
 RS11\_SALT STD. STANDARD; PRT: 9 AA.  
 AC 054296;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE 30S RIBOSOMAL PROTEIN S11 (FRAGMENT).  
 GN RPSK.  
 OS Salmonella typhimurium.  
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 CC Salmonella.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2;  
 RA Bjorkman J., Hughes D., Andersson D.;  
 RL Submitted (Jan-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: S11 PLAYS AN ESSENTIAL ROLE FOR THE SELECTION OF THE  
 CC CORRECT TENA IN PROTEIN BIOSYNTHESIS. IT IS LOCATED ON THE LARGE  
 CC LOBE OF THE SMALL SUBUNIT (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE SLP FAMILY OF RIBOSOMAL PROTEINS.  
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 CC EMBL: AJ223236; CNA11202.1;  
 DR STYGENE; SG10702; RPSK.  
 DR INTERPRO: IPR001971;  
 DR PROSITE: PS00054; RIBOSOMAL\_S11; PARTIAL.  
 KW Ribosomal protein.  
 FT NON-TER 1 1  
 FT SEQUENCE 9 AA; 1139 MW; 7A5B14033277774 CRC64;  
 SQ

Query Match 22.9%; Score 19; DB 1; Length 9;  
 Best Local Similarity 42.9%; Pred. No. 8.9e+04;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 OY 5 CKPOYTR 11  
 1 1 1  
 DB 1 CRPKKR 7

RESULT 11  
 PED1\_HYDAT STD. STANDARD; PRT: 13 AA.  
 AC P80578;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE PEDIN.  
 OS Hydra attenuata (Hydra) (Hydra vulgaris).  
 CC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;  
 CC Hydridae; Hydra.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96232307; PubMed=8674432;  
 RA Hoffmeister S.A.H.;  
 RT "Isolation and characterization of two new morphogenetically active  
 RT peptides from Hydra vulgaris.";  
 RL Development 122:1941-1948(1996).  
 CC -1- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT  
 CC DEVELOPMENT.  
 KW Morphogen.  
 FT NON-TER 13 13  
 FT SEQUENCE 13 AA; 1512 MW; 6F5266E3F7632CB CRC64;  
 SQ

Query Match 22.9%; Score 19; DB 1; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 ECKPOV 9  
 1 1 1  
 DB 2 ELRPEV 7

RESULT 12  
 OXYT\_RAUTL STD. STANDARD; PRT: 9 AA.  
 AC P42994;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE GLUTINOCIN.  
 OS Raja clavata (Thornback ray).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 CC Elasmobranchii; Squala; Hyposqualae; Pristiorajae; Batoidae;  
 CC Rajiformes; Rajidae; Raja.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=66123415; PubMed=5880565;  
 RA Achter R., Chauvet J., Chauvet M.-T., Crepy D.;  
 RT "Phylogeny of neurohypophyseal peptides: isolation of a new hormone,  
 RT glutinocin (Ser 4-Gln 8-oxytocin) present in a cartilaginous fish,  
 RT the ray (Raja clavata).";  
 RL Blochm. Biophys. Acta 107:393-396(1965).  
 CC -1- FUNCTION: ANTI-DIURETIC HORMONE.  
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 CC INTERPRO: IPR000981;  
 DR PFM: PF00220; hormone4; 1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT MOD\_RES 1 1  
 FT DISULFID 9 9  
 FT SEQUENCE 9 AA; 984 MW; 17E9C76E845B04B CRC64;  
 SQ

Query Match 21.1%; Score 17.5; DB 1; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 8.9e+04;

Matches 4; Conservative 1; Mismatches 2; Indels 1; Gaps 1;  
 OY 1 YTAECKPO 8  
 1 1 1 1  
 DB 2 YISNC-PO 8

RESULT 13  
 BPP2\_BOTIN STANDARD; PRT; 10 AA.

AC P01022; 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE BRADYKININ-POTENTIATING PEPTIDE 10B (ANGIOTENSIN-CONVERTING ENZYME INHIBITOR V-6-II).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae; Viperidae; Crotalinae; Bothrops.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-VENOM;  
 RX MEDLINE=72118526; PubMed=4334402;  
 RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R., Kocay O.;  
 RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. Isolation, elucidation of structure, and synthesis."  
 RL Biochemistry 10:4033-4039(1971).  
 CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.  
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.  
 DR PIR: A01255; XAVI6B.  
 KM Hypotensive agent; Venom.  
 FT MOD.RES 1  
 SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match  
 Best Local Similarity 20.5%; Score 17; DB 1; Length 10;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 KPOV 9  
 1 1 1 1  
 DB 5 RPOI 8

RESULT 14  
 BPP3\_BOTIN STANDARD; PRT; 11 AA.

AC P30423; 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE BRADYKININ-POTENTIATING PEPTIDE 54,3,2 (10C) (ANGIOTENSIN-CONVERTING ENZYME INHIBITOR).  
 OS Bothrops insularis (Island Jararaca) (Queimada Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae; Viperidae; Crotalinae; Bothrops.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-VENOM;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom."  
 RL J. Protein Chem. 9:221-227(1990).  
 DE -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.  
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.

DR PIR: C37196; C37196.  
 KM Hypotensive agent; Venom.  
 FT MOD.RES 1  
 SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741773 CRC64;

Query Match  
 Best Local Similarity 20.5%; Score 17; DB 1; Length 11;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 KPOV 9  
 1 1 1 1  
 DB 6 RPOI 9

RESULT 15  
 BPP4\_BOTIN STANDARD; PRT; 11 AA.

AC P30424; 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE BRADYKININ-POTENTIATING PEPTIDE 54,1,2 (ANGIOTENSIN-CONVERTING ENZYME INHIBITOR).  
 OS Bothrops insularis (Island Jararaca) (Queimada Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae; Viperidae; Crotalinae; Bothrops.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-VENOM;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom."  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.  
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.  
 DR PIR: D37195; D37195.  
 KM Hypotensive agent; Venom.  
 FT MOD.RES 1  
 SQ SEQUENCE 11 AA; 1143 MW; 20BBB13C7741773 CRC64;

Query Match  
 Best Local Similarity 20.5%; Score 17; DB 1; Length 11;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 KPOV 9  
 1 1 1 1  
 DB 6 RPOI 9

Search completed: March 6, 2001, 09:50:33  
 Job time: 110 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 6, 2001, 09:48:28 ; Search time 19.79 Seconds

(Without alignments)  
88.839 Million cell updates/sec

Title: US-09-081-522-8

Sequence: 1 YTAECKPQVTRGDVF 15

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 2289

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_15:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	39.8	11	9	Q38415
2	30	36.1	15	2	O69142
3	25	30.1	10	6	O9N1X1
4	24	28.9	11	2	O48933
5	24	28.9	15	2	O9X637
6	24	28.9	15	2	O9X635
7	22	26.5	15	11	O9QV00
8	21	25.3	7	10	P82445
9	21	25.3	11	7	O77871
10	21	25.3	11	7	O77872
11	21	25.3	11	7	O77873
12	21	25.3	12	4	O9UC37
13	21	25.3	13	2	P74844
14	21	25.3	15	4	O9Y4Z9
15	20	24.1	10	10	P82438
16	20	24.1	14	10	P82322
17	20	24.1	15	4	O9UCX1
18	20	24.1	15	12	O97092
19	20	24.1	15	12	O97094

20	19	22.3	13	8	Q9T2U1	Q9T2U1 bos taurus
21	19	22.9	14	8	O9MR66	O9MR66 hordeum mur
22	19	22.9	14	12	O89818	O89818 murine min
23	19	22.9	15	5	O9TWD5	O9TWD5 locusta mig
24	19	22.9	15	8	O9T355	O9T355 synagrops b
25	19	22.9	15	13	O9PR29	O9PR29 micropogonl
26	18.5	22.3	15	5	O9TXC8	O9TXC8 locusta mig
27	18	21.7	9	2	O9R735	O9R735 streptomyce
28	18	21.7	10	2	O9ZIB1	O9ZIB1 clostridium
29	18	21.7	12	4	O9UMZ8	O9UMZ8 homo sapien
30	18	21.7	12	10	O41856	O41856 zea mays (m
31	18	21.7	12	11	O9Q2Y4	O9Q2Y4 mus musculu
32	18	21.7	15	2	O9R399	O9R399 micrococcus
33	18	21.7	15	4	O9UC67	O9UC67 homo sapien
34	18	21.7	15	7	O19468	O19468 mus musculu
35	17	20.5	8	2	O9S6D5	O9S6D5 escherichia
36	17	20.5	9	4	O16386	O16386 homo sapien
37	17	20.5	9	4	O99867	O99867 homo sapien
38	17	20.5	11	7	O78119	O78119 oreochromis
39	17	20.5	11	13	O90735	O90735 gallus gall
40	17	20.5	13	2	O9X9D7	O9X9D7 bacillus ha
41	17	20.5	13	4	O15537	O15537 homo sapien
42	17	20.5	13	12	O81769	O81769 hepatitis c
43	17	20.5	13	12	O81770	O81770 hepatitis c
44	17	20.5	13	12	O81781	O81781 hepatitis c
45	17	20.5	13	12	O81761	O81761 hepatitis c

## ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	11 AA.
ID	O38415			
AC	O38415			
DT	01-NOV-1996 (TEMBLrel. 01, Created)			
DT	01-NOV-1996 (TEMBLrel. 01, Last sequence update)			
DT	01-NOV-1998 (TEMBLrel. 08, Last annotation update)			
DE	ANP1 PROTEIN (FRAGMENT).			
OS	Bacteriophage P7.			
OC	Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae.			
OX	NCBI_taxid:10682;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-90335963; PubMed-1696181;			
RA	Citron M., Schuster H.;			
RT	"The c4 repressors of bacteriophages P1 and P7 are antisense RNAs."			
RL	Cell 62:591-598(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE-92319637; PubMed-1620606;			
RT	Citron M., Schuster H.;			
RT	"The c4 repressor of bacteriophage P1 is a processed 77 base antisense RNA."			
RL	Nucleic Acids Res. 20:3085-3090(1992).			
DR	EMBL; M35139; AAA32437.1; -			
FT	NON TER			
SO	SEQUENCE			
Query Match	39.8%;	Score 33;	DB 9;	Length 11;
Best Local Similarity	56.7%;	Pred. No. 15;		
Matches	6;	Conservative	1;	Mismatches 2;
				Indels 0;
				Gaps 0;
OY	6 KPOVTRGDV 14			
Db	3 KPLVTRNDI 11			
RESULT	2			
ID	O69142	PRELIMINARY;	PRT;	15 AA.
AC	O69142;			

DT 01-AUG-1998 (TREMblrel. 07, Created)  
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)  
 DT 01-AUG-1998 (TREMblrel. 07, Last annotation update)  
 DE PROTEIN SIC (FRAGMENT).  
 GN STC.  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 OC Streptococcus.  
 RX NCBI\_TaxID=1314;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-API;  
 RA Berge A., Rasmussen M., Bjorck L.;  
 RL Infect. Immun. 0:0-0(1998).  
 DR EMBL; AF064540; AAC38769.1; -  
 FT NON\_TER 1 1  
 SQ SEQUENCE 15 AA; 1552 MW; 87655F847401FF CRC64;

Query Match  
 Best Local Similarity 36.1%; Score 30; DB 2; Length 15;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 CRQVT 10  
 DB 3 CRPVT 8

RESULT 3  
 Q9NIX1 PRELIMINARY; PRT; 10 AA.

AC Q9NIX1  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
 DE ALCOHOL DEHYDROGENASE 3 (FRAGMENT).  
 GN ADH3.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteria; Perissodactyla; Equidae; Equus.  
 RX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20082971; PubMed=10613847;  
 RA Caetano A.R., Shue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,  
 RT Bowlin A.T., Murray J.D.;  
 RL "A comparative gene map of the horse (Equus caballus).";  
 RL Genome Res. 9:1239-1249(1999).  
 DR EMBL; AF134056; AAF31299.1; -  
 FT NON\_TER 1 1  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1144 MW; C4EA25676B02D6DD CRC64;

Query Match  
 Best Local Similarity 30.1%; Score 25; DB 6; Length 10;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 TAECKPQVT 10  
 DB 2 TAEVPEPVT 10

RESULT 4  
 Q48933 PRELIMINARY; PRT; 11 AA.  
 AC Q48933; P77701; Q48932;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
 DE ALKYL HYDROPEROXIDE REDUCTASE C (FRAGMENT).  
 GN AHP.  
 OS Mycobacterium bovis.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 RX NCBI\_TaxID=1765;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC35728; AND ATCC35727;  
 RA Zhang Y., Deric V.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC35735;  
 RX MEDLINE=96236622; PubMed=8655566;  
 RA Dhandayuthapani S., Zhang Y., Deric V.;  
 RT "Oxidative stress response and its role in sensitivity to isoniazid in  
 Mycobacteria: characterization and inducibility of ahpC by peroxides  
 in Mycobacterium smegmatis and lack of expression in M. aurum and M.  
 tuberculosis";  
 RL J. Bacteriol. 178:3641-3649(1996).  
 DR EMBL; U58031; AAB00320.1; -  
 DR EMBL; U57979; AAB9830.1; -  
 DR EMBL; U57978; AAB9829.1; -  
 DR EMBL; U57762; AAB00317.1; -  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1231 MW; 45509E3A87041A7 CRC64;

Query Match  
 Best Local Similarity 28.9%; Score 24; DB 2; Length 11;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 PQTGVDY 15  
 DB 2 PLRTGDDP 10

RESULT 5  
 Q9X637 PRELIMINARY; PRT; 15 AA.

AC Q9X637  
 DT 01-NOV-1999 (TREMblrel. 12, Created)  
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
 DE MERT (FRAGMENT).  
 GN MERT.  
 OS Klebsiella oxytoca.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Klebsiella.  
 RX NCBI\_TaxID=571;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=509H;  
 RX MEDLINE=97206220; PubMed=9055422;  
 RA Liebert C.A., Wieman J., Smith T., Summers A.O.;  
 RT "Phylogeny of mercury resistance (mer) operons of gram-negative  
 bacteria isolated from the fecal flora of primates";  
 RL Appl. Environ. Microbiol. 63:1066-1076(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=509H;  
 RX MEDLINE=96027386; PubMed=9361435;  
 RA Wieman J., Liebert C.A., Smith T., Summers A.O.;  
 RT "Association of mercury resistance with antibiotic resistance in the  
 gram-negative fecal bacteria of primates";  
 RL Appl. Environ. Microbiol. 63:4494-4503(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=509H;  
 RX Wieman J., Liebert C.A., Smith T., Summers A.O.;  
 RT "15-bp tandem repeats occur at a sharp transition in gc content in the  
 mer operon";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF131272; AAD37141.1; -  
 FT NON\_TER 15 15



SQL SEQUENCE 15 AA; 1492 MW; 65BFCFC9827A585D CRC64;

Query Match 28.9%; Score 24; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 8.5e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 6 KPOVTRGDV 15  
DB 3 EPONGRGALF 12

RESULT 6  
ID 09X635 PRELIMINARY; PRT; 15 AA.

AC 09X635; 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DE MERT (FRAGMENT).  
CN MERT.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-390;  
RA MEDLINE-97208220; PubMed-9055422;  
RX Liebert C.A., Wireman J., Smith T., Summers A.O.;  
RT Phylogeny of mercury resistance (mer) operons of gram-negative  
bacteria isolated from the fecal flora of primates."  
RL Appl. Environ. Microbiol. 63:1066-1076 (1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-390;  
RA MEDLINE-98027386; PubMed-9361435;  
RX Wireman J., Liebert C.A., Smith T., Summers A.O.;  
RT "Association of mercury resistance with antibiotic resistance in the  
gram-negative fecal bacteria of primates."  
RL Appl. Environ. Microbiol. 63:4494-4503 (1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-390;  
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;  
RT "15-bp tandem repeats occur at a sharp transition in gc content in the  
mer operon."  
RL EMBL; AF131271; AAD37139.1;  
FT NON TER 15 15  
SQ SEQUENCE 15 AA; 1492 MW; 65BFCFC9827A585D CRC64;

Query Match 28.9%; Score 24; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 8.5e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 6 KPOVTRGDV 15  
DB 3 EPONGRGALF 12

RESULT 7  
ID 09Y000 PRELIMINARY; PRT; 15 AA.

AC 09Y000; 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DE EOSINOPHIL CATIONIC PROTEIN (FRAGMENT).  
OS Rattus sp.  
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10113;

RP [1]  
RX MEDLINE-95375557; PubMed-7647580;  
RA Watanabe K., Nittoh T., Suzuki T., Kitch A., Mue S., Ohuchi K.;  
RT "Isolation and partial characterization of eosinophil granule proteins  
in rats-eosinophil cationic protein and major basic protein."  
RL Int. Arch. Allergy Immunol. 108:11-18 (1995).  
SQ SEQUENCE 15 AA; 1785 MW; 2AF6D9C12EBD794 CRC64;

Query Match 26.5%; Score 22; DB 11; Length 15;  
Best Local Similarity 50.0%; Pred. No. 2e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTAECK 5  
DB 6 FTGHCK 11

RESULT 8  
ID P82445 PRELIMINARY; PRT; 7 AA.

AC P82445; 01-JUN-2000 (TREMBlrel. 14, Created)  
DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)  
DE 10 KDA CELL WALL PROTEIN (FRAGMENT).  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; easterids I;  
OC Solanales; Solanales; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE.  
RC STRAIN-CV. PETIT HAVANA;  
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
RJ Woljasek P., Bolwell G.P.;  
RT "Proteomic study of secondary cell wall proteins from transformed  
tobacco culture."  
RL Planta 200:0-0 (2000).  
CC -1- SUBCELLULAR LOCATION: CELL WALL.  
CC -1- TISSUE SPECIFICITY: XYLEM.  
KW Cell wall.  
FT NON TER 7 7  
SQ SEQUENCE 7 AA; 758 MW; 69D2C1E862D1B2A0 CRC64;

Query Match 25.3%; Score 21; DB 10; Length 7;  
Best Local Similarity 71.4%; Pred. No. 3.7e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 9 VTRGDV 15  
DB 1 VTVGHVF 7

RESULT 9  
ID 077871 PRELIMINARY; PRT; 11 AA.

AC 077871; 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DE MHC CLASS II B LOCUS 1 (FRAGMENT).  
OS Oreochromis niloticus (Nile tilapia).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorphi; Acanthopterygii; Percomorphi; Perciformes; Labroidae;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., Figuerola F., Vincsek V., Zaleska-Rutczynska Z.,  
 RP Sueltmann H., Figuerola F., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid Mhc  
 class II B loci."  
 RL Genetics 149:1527-1547(1998).  
 DR EMBL: AF049980; AAC41319.1; -  
 KW MHC.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1133 MW; 283248EC3EB72728 CRC64;

Query Match 25.3%; Score 21; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CKP 7  
 DB 7 CKP 9

RESULT 10  
 ID 077872 PRELIMINARY; PRT: 11 AA.  
 AC 077872;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DE MHC CLASS II B LOCUS 1 (FRAGMENT).  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidel;  
 OC Cichlidae; Oreochromis.  
 RX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., McAndrew B., Vincsek V., Zaleska-Rutczynska Z.,  
 RP Sueltmann H., Figuerola F., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid Mhc  
 class II B loci."  
 RL Genetics 149:1527-1547(1998).  
 DR EMBL: AF049981; AAC41320.1; -  
 KW MHC.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1133 MW; 283248EC3EB72728 CRC64;

Query Match 25.3%; Score 21; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CKP 7  
 DB 7 CKP 9

RESULT 11  
 ID 077873 PRELIMINARY; PRT: 11 AA.  
 AC 077873;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DE MHC CLASS II B LOCUS 1 (FRAGMENT).  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidel;  
 OC Cichlidae; Oreochromis.

OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., McAndrew B., Vincsek V., Zaleska-Rutczynska Z.,  
 RP Sueltmann H., Figuerola F., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid Mhc  
 class II B loci."  
 RL Genetics 149:1527-1547(1998).  
 DR EMBL: AF049982; AAC41321.1; -  
 KW MHC.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1133 MW; 283248EC3EB72728 CRC64;

Query Match 25.3%; Score 21; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CKP 7  
 DB 7 CKP 9

RESULT 12  
 ID 09UC37 PRELIMINARY; PRT: 12 AA.  
 AC 09UC37;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE ALPHA B CRYSTALLIN FRAGMENT 5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=92218434; PubMed=1560006;  
 RA Kato K., Shiohara H., Goto S., Inaguma Y., Morishita R., Asano T.;  
 RT "Copurification of small heat shock protein with alpha B crystallin  
 from human skeletal muscle."  
 RL J. Biol. Chem. 267:7718-7725(1992).  
 SQ SEQUENCE 12 AA; 1268 MW; D37BD529CC1B2CD CRC64;

Query Match 25.3%; Score 21; DB 4; Length 12;  
 Best Local Similarity 71.4%; Pred. No. 2.4e+03;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 ECKPYVT 10  
 DB 1 ECKPYVT 7

RESULT 13  
 ID P74844 PRELIMINARY; PRT: 13 AA.  
 AC P74844;  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DE SIGMA FACTOR (FRAGMENT).  
 GN FLIA.  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmonella.  
 RX NCBI\_TaxID=602;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168-94;  
 RX MEDLINE=97311993; PubMed=9168604;

RA Burnens A.P., Stanley J., Sack R., Hunziker P., Brodard I.,  
 RA Nicolet J.,  
 RT "The flagellin N-methylase gene flib and an adjacent serovar-specific  
 RT IS200 element in *Salmonella typhimurium*.";  
 RL Microbiology 143:1539-1547(1997).  
 DR EMBL; Z67749; CAB91563.1; -;  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1459 MW; 99199C0161421DC1 CRC64;

Query Match 25.3%; Score 21; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTAE 4  
 |||  
 Db 5 YTAE 8

## RESULT 14

O9Y429 PRELIMINARY; PRT; 15 AA.  
 AC O9Y429;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE FANCA PROTEIN (FRAGMENT).  
 GN FANCA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA D'Apollito M., Tanzano L., Savino M., Rommens J., Zélande L.,  
 RA Savola A.;  
 RT "Differential expression of FANCA and FANCC genes in human tissues and  
 RT alternative splicing of FANCA transcripts.";  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ11189; CAB46099.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 15 AA; 1590 MW; 8732D75A24DCA4F0 CRC64;

Query Match 25.3%; Score 21; DB 4; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 3e+03;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 CRPQVTRG 12  
 |||  
 Db 8 CGPSHLRG 15

## RESULT 15

P82438 PRELIMINARY; PRT; 10 AA.  
 AC P82438;  
 DT 01-JUN-2000 (TREMBLrel. 14, Created)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE 50 KDA CELL WALL PROTEIN (FRAGMENT).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;  
 OC Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_Taxid=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN-CV. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 tobacco culture.";

RL Planta 0:0-0(2000).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1126 MW; C68E32486AF77B46 CRC64;

Query Match 24.1%; Score 20; DB 10; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 3e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 PQVTRGDV 14  
 |||  
 Db 2 PQVTRGVN 9

Search completed: March 6, 2001, 09:50:22  
 Job time: 114 sec

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